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(54) Title: UBIQUITIN CONJUGATION PROTEINS

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1  MSSTSSSKRAPTTATQRLKODYLRICKKDPVP UCSP-1
1  MATKQAHK-----RLTKEYYKLMVENPPP g397581
1  -----YK-----RLMKELYLA LQKNPF E g1749704

31  YICAEPLPSNILEWHYVVVRGPPEMTPYEGGY UCSP-1
24  YILARP NEDNILEWHYIITGPADTPYKGGQ g397581
18  LVD A K P A T E N I L E W H Y I I T G P P D T P Y E G G Q g1749704

61  YH GK L I F P R E F P F K P P S I Y M I T P N G R F K C N UCSP-1
54  Y H G T L T F P S D Y P Y K P P A I R M I T P N G R F K P N g397581
48  Y H G T L I F P P D Y P F K P P A I R M I T P S G R F Q T N g1749704

91  T R L C L S I T D F H P D T W N P A W S V S T I L T G L L S UCSP-1
84  T R L C L S M S D Y H P D T W N P G W S V S T I L N G L L S g397581
78  T R L C L S F S D F H P K S W N P S W M V S T I L V G L V S g1749704

121 F M V E K G P T L G S I E T S D F T K R Q L A V Q S L A F N UCSP-1
114 F M T S D E A T T G S I T T S D H Q K K T L A R N S I S Y N g397581
108 F M T S D E I T T G G I V T S E S T R R T Y A K D T K R F N g1749704

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## (57) Abstract

The present invention provides a human ubiquitin conjugation system protein (UCSP) and polynucleotides which encode UCSP. The invention also provides expression vectors, host cells, agonists, antisense molecules, antibodies, or antagonists. The invention also provides methods for treating disorders associated with expression of UCSP.

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## UBIQUITIN CONJUGATION PROTEINS

### TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of two new ubiquitin conjugation system proteins and to the use of these sequences in the diagnosis, prevention, and  
5 treatment of cancer, immune disorders, smooth muscle disorders, and viral infections.

### BACKGROUND ART

The ubiquitin conjugation system (UCS) is a major pathway for the degradation of cellular proteins in eukaryotic cells and in some bacteria. The UCS mediates the elimination of abnormal proteins and regulates the half-lives of important regulatory proteins that control  
10 cellular processes such as gene transcription and cell cycle progression. The UCS is implicated in the degradation of mitotic cyclic kinases, oncoproteins, tumor suppressor genes such as p53, viral proteins, cell surface receptors associated with signal transduction, transcriptional regulators, and mutated or damaged proteins (Ciechanover, A. (1994) Cell 79:13-21).

The process of ubiquitin conjugation and protein degradation occurs in four principal  
15 steps (Jentsch, S. (1992) Annu. Rev. Genet. 26:179-207). First ubiquitin (Ub), a small, heat stable protein (76 amino acids) is activated by a ubiquitin-activating enzyme (E1) in an ATP dependent reaction which binds the C-terminus of Ub to the thiol group of an internal cysteine residue in E1. Second, activated Ub is transferred to one of several Ub-conjugating enzymes (E2). Different ubiquitin-dependent proteolytic pathways employ structurally similar, but distinct  
20 ubiquitin-conjugating enzymes that are associated with recognition subunits which direct them to proteins carrying a particular degradation signal. E2 then links the Ub molecule through its C-terminal glycine to an internal lysine (acceptor lysine) of a target protein. Additional Ub molecules may be added forming a multi-Ub chain structure. The ubiquitinated protein is then recognized and degraded by proteasome, a large, multisubunit proteolytic enzyme complex, and  
25 Ub is released for reutilization.

Prior to activation, Ub is usually expressed as a fusion protein composed of an N-terminal ubiquitin and a C-terminal extension protein (CEP), or as a polyubiquitin protein with Ub monomers attached head to tail. CEPs bear similarities to a variety of nucleic acid binding regulatory proteins. Most are highly basic with up to 30% lysine and arginine residues, and many  
30 have nucleic acid-binding, zinc-finger domains (Monia, B.P. et al. (1989) J. Biol. Chem. 264:4093-4103). These Ub-CEP fusion proteins are rapidly processed by C-terminal hydrolases which cleave Ub from the C-terminal side releasing free Ub for the UCS. The fusion of Ub with CEPs may allow co-regulation of the UCS with the translational activity of the cell. Processing

of the CEPs may also be required to localize CEPs or Ub to specific cellular sites where they carry out their function (Monia et al., supra).

The E2 (Ub-conjugating) enzymes are important for substrate specificity in different UCS pathways. All E2s have a conserved domain of approximately 16 kDa called the UBC domain  
5 that is at least 35% identical in all E2s and contains a centrally located cysteine residue required for ubiquitin-enzyme thiolester formation (Jentsch, supra). A highly conserved proline-rich element is located N-terminal to the active cysteine residue. Structural variations beyond this conserved domain are used to classify the E2 enzymes. Class I E2s consist almost exclusively of the conserved UBC domain. Class II E2s have various unrelated C-terminal extensions that  
10 contribute to substrate specificity and cellular localization. Yeast class II enzymes UBC2 and UBC3 have highly acidic C-terminal extensions that promote interactions with basic substrates such as histones. Yeast UBC6 has a hydrophobic signal-anchor sequence that localizes the protein to the endoplasmic reticulum.

The discovery of new ubiquitin conjugation system proteins and the polynucleotides  
15 encoding them satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment or prevention of cancer, immune disorders, smooth muscle disorders, and viral infections.

### DISCLOSURE OF THE INVENTION

The present invention features two new human ubiquitin-conjugation system proteins  
20 hereinafter designated as UCSP-1 and UCSP-2, and collectively as UCSP, and characterized as having similarity to other ubiquitin-conjugation system proteins.

Accordingly, the invention features a substantially purified UCSP-1 and UCSP-2 having the amino acid sequences shown in SEQ ID NO:1 and SEQ ID NO:3, respectively.

One aspect of the invention features isolated and substantially purified polynucleotides  
25 that encode UCSP-1 and UCSP-2. In a particular aspect, the polynucleotides are the nucleotide sequences of SEQ ID NO:2 and SEQ ID NO:4, respectively.

The invention also relates to polynucleotide sequences comprising the complement of SEQ ID NO:2 or SEQ ID NO:4 or variants thereof. In addition, the invention features polynucleotide sequences which hybridize under stringent conditions to SEQ ID NO:2 or SEQ ID  
30 NO:4.

The invention additionally features fragments of the polynucleotides encoding UCSP, expression vectors and host cells comprising polynucleotides that encode UCSP and a method for producing UCSP using the vectors and host cells. The present invention also features antibodies

which bind specifically to UCSP, and pharmaceutical compositions comprising substantially purified UCSP. The invention also features agonists and antagonists of UCSP. The invention also provides methods for treating disorders associated with expression of UCSP by administration of UCSP and methods for detection of polynucleotides encoding ubiquitin-  
5 conjugation proteins in a biological sample using the complement of the polynucleotide encoding UCSP.

### BRIEF DESCRIPTION OF DRAWINGS

Figures 1A, 1B and 1C show the amino acid sequence (SEQ ID NO:1) and nucleic acid sequence (SEQ ID NO:2) of UCSP-1. The alignment was produced using MacDNASIS PRO™  
10 software (Hitachi Software Engineering Co., Ltd., San Bruno, CA).

Figures 2A, 2B, 2C, and 2D, show the amino acid sequence (SEQ ID NO:3) and nucleic acid sequence (SEQ ID NO:4) of UCSP-2. The alignment was produced using MacDNASIS PRO™ software.

Figures 3A and 3B show the amino acid sequence alignments among UCSP-1 (SEQ ID  
15 NO:1), and the ubiquitin-conjugating enzyme, UBC6, from Saccharomyces cerevisiae (GI 397581; SEQ ID NO:5) and Shizosaccharomyces pombe (GI 1749704; SEQ ID NO:6). The alignment was produced using the multisequence alignment program of DNASTAR™ software (DNASTAR Inc, Madison WI).

Figures 4A and 4B shows the amino acid sequence alignments among UCSP-2 (SEQ ID  
20 NO:3), a ubiquitin-like CEP protein from Caenorhabditis elegans (GI 1279278; SEQ ID NO:7), and cow (GI 998680; SEQ ID NO:8). The alignment was produced using the multisequence alignment program of DNASTAR™ software.

Figures 5A and 5B show the hydrophobicity plots (MacDNASIS PRO™) for UCSP-1, SEQ ID NO:1; and UBC6 from S. cerevisiae, SEQ ID NO:5, and S. pombe, SEQ ID NO:6. The  
25 positive X axis reflects amino acid position, and the negative Y axis, hydrophobicity.

Figures 6A and 6B show the hydrophobicity plots (MacDNASIS PRO™) for UCSP-2, SEQ ID NO:3; and the ubiquitin-like CEP protein from C. elegans, SEQ ID NO:7). The positive X axis reflects amino acid position, and the negative Y axis, hydrophobicity.

### MODES FOR CARRYING OUT THE INVENTION

30 Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular methodology, protocols, cell lines, vectors, and reagents described as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to

limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms “a”, “an”, and “the” include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to “a host cell” includes a plurality of such host cells, reference to the  
5 “antibody” is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can  
10 be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are reported in the publications which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate  
15 such disclosure by virtue of prior invention.

#### DEFINITIONS

“Nucleic acid sequence” as used herein refers to an oligonucleotide, nucleotide, or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand.  
20 Similarly, “amino acid sequence” as used herein refers to an oligopeptide, peptide, polypeptide, or protein sequence, and fragments or portions thereof, and to naturally occurring or synthetic molecules.

Where “amino acid sequence” is recited herein to refer to an amino acid sequence of a naturally occurring protein molecule, “amino acid sequence” and like terms, such as  
25 “polypeptide” or “protein” are not meant to limit the amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule.

“Peptide nucleic acid”, as used herein, refers to a molecule which comprises an oligomer to which an amino acid residue, such as lysine, and an amino group have been added. These small molecules, also designated anti-gene agents, stop transcript elongation by binding to their  
30 complementary strand of nucleic acid (Nielsen, P.E. et al. (1993) Anticancer Drug Des. 8:53-63).

UCSP, as used herein, refers to the amino acid sequences of substantially purified UCSP obtained from any species, particularly mammalian, including bovine, ovine, porcine, murine, equine, and preferably human, from any source whether natural, synthetic, semi-synthetic, or

recombinant.

“Consensus”, as used herein, refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, or which has been extended using XL-PCR™ (Perkin Elmer, Norwalk, CT) in the 5' and/or the 3' direction and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte clone using the GELVIEW™ Fragment Assembly system (GCG, Madison, WI), or which has been both extended and assembled.

A “variant” of UCSP, as used herein, refers to an amino acid sequence that is altered by one or more amino acids. The variant may have “conservative” changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More rarely, a variant may have “nonconservative” changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, DNASTAR software.

A “deletion”, as used herein, refers to a change in either amino acid or nucleotide sequence in which one or more amino acid or nucleotide residues, respectively, are absent.

An “insertion” or “addition”, as used herein, refers to a change in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid or nucleotide residues, respectively, as compared to the naturally occurring molecule.

A “substitution”, as used herein, refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

The term “biologically active”, as used herein, refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, “immunologically active” refers to the capability of the natural, recombinant, or synthetic UCSP, or any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term “agonist”, as used herein, refers to a molecule which, when bound to UCSP, causes a change in UCSP which modulates the activity of UCSP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to UCSP.

The terms “antagonist” or “inhibitor”, as used herein, refer to a molecule which, when bound to UCSP, blocks or modulates the biological or immunological activity of UCSP. Antagonists and inhibitors may include proteins, nucleic acids, carbohydrates, or any other

molecules which bind to UCSP.

The term “modulate”, as used herein, refers to a change or an alteration in the biological activity of UCSP. Modulation may be an increase or a decrease in protein activity, a change in binding characteristics, or any other change in the biological, functional or immunological  
5 properties of UCSP.

The term “mimetic”, as used herein, refers to a molecule, the structure of which is developed from knowledge of the structure of UCSP or portions thereof and, as such, is able to effect some or all of the actions of ubiquitin conjugation system protein-like molecules.

The term “derivative”, as used herein, refers to the chemical modification of a nucleic  
10 acid encoding UCSP or the encoded UCSP. Illustrative of such modifications would be replacement of hydrogen by an alkyl, acyl, or amino group. A nucleic acid derivative would encode a polypeptide which retains essential biological characteristics of the natural molecule.

The term “substantially purified”, as used herein, refers to nucleic or amino acid sequences that are removed from their natural environment, isolated or separated, and are at least  
15 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated.

“Amplification” as used herein refers to the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction (PCR) technologies well known in the art (Dieffenbach, C.W. and G.S. Dveksler (1995) PCR Primer, a Laboratory  
20 Manual, Cold Spring Harbor Press, Plainview, NY).

The term “hybridization”, as used herein, refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

The term “hybridization complex”, as used herein, refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary  
25 G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen bond in an antiparallel configuration. A hybridization complex may be formed in solution (e.g.,  $C_0t$  or  $R_0t$  analysis) or between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., membranes, filters, chips,  
30 pins or glass slides to which cells have been fixed for in situ hybridization).

The terms “complementary” or “complementarity”, as used herein, refer to the natural binding of polynucleotides under permissive salt and temperature conditions by base-pairing. For example, for the sequence “A-G-T” binds to the complementary sequence “T-C-A”.



Complementarity between two single-stranded molecules may be "partial", in which only some of the nucleic acids bind, or it may be complete when total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands.

- 5 This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands.

The term "homology", as used herein, refers to a degree of complementarity. There may be partial homology or complete homology (i.e., identity). A partially complementary sequence is one that at least partially inhibits an identical sequence from hybridizing to a target nucleic  
10 acid; it is referred to using the functional term "substantially homologous." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the binding (i.e., the hybridization) of a completely homologous sequence or probe to  
15 the target sequence under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (i.e., selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% identity); in the absence of  
20 non-specific binding, the probe will not hybridize to the second non-complementary target sequence.

As known in the art, numerous equivalent conditions may be employed to comprise either low or high stringency conditions. Factors such as the length and nature (DNA, RNA, base composition) of the sequence, nature of the target (DNA, RNA, base composition, presence in  
25 solution or immobilization, etc.), and the concentration of the salts and other components (e.g., the presence or absence of formamide, dextran sulfate and/or polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions of either low or high stringency different from, but equivalent to, the above listed conditions.

The term "stringent conditions", as used herein, is the "stringency" which occurs within a  
30 range from about  $T_m - 5^\circ\text{C}$  ( $5^\circ\text{C}$  below the melting temperature ( $T_m$ ) of the probe) to about  $20^\circ\text{C}$  to  $25^\circ\text{C}$  below  $T_m$ . As will be understood by those of skill in the art, the stringency of hybridization may be altered in order to identify or detect identical or related polynucleotide sequences.

The term "antisense", as used herein, refers to nucleotide sequences which are complementary to a specific DNA or RNA sequence. The term "antisense strand" is used in reference to a nucleic acid strand that is complementary to the "sense" strand. Antisense molecules may be produced by any method, including synthesis by ligating the gene(s) of interest in a reverse orientation to a viral promoter which permits the synthesis of a complementary strand. Once introduced into a cell, this transcribed strand combines with natural sequences produced by the cell to form duplexes. These duplexes then block either the further transcription or translation. In this manner, mutant phenotypes may be generated. The designation "negative" is sometimes used in reference to the antisense strand, and "positive" is sometimes used in reference to the sense strand.

The term "portion", as used herein, with regard to a protein (as in "a portion of a given protein") refers to fragments of that protein. The fragments may range in size from four amino acid residues to the entire amino acid sequence minus one amino acid. Thus, a protein "comprising at least a portion of the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:3" encompasses the full-length human UCSP and fragments thereof.

"Transformation", as defined herein, describes a process by which exogenous DNA enters and changes a recipient cell. It may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed and may include, but is not limited to, viral infection, electroporation, lipofection, and particle bombardment. Such "transformed" cells include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome. They also include cells which transiently express the inserted DNA or RNA for limited periods of time.

The term "antigenic determinant", as used herein, refers to that portion of a molecule that makes contact with a particular antibody (i.e., an epitope). When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as antigenic determinants. An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The terms "specific binding" or "specifically binding", as used herein, in reference to the interaction of an antibody and a protein or peptide, mean that the interaction is dependent upon

the presence of a particular structure (i.e., the antigenic determinant or epitope) on the protein; in other words, the antibody is recognizing and binding to a specific protein structure rather than to proteins in general. For example, if an antibody is specific for epitope "A", the presence of a protein containing epitope A (or free, unlabeled A) in a reaction containing labeled "A" and the  
5 antibody will reduce the amount of labeled A bound to the antibody.

The term "sample", as used herein, is used in its broadest sense. A biological sample suspected of containing nucleic acid encoding UCSP or fragments thereof may comprise a cell, chromosomes isolated from a cell (e.g., a spread of metaphase chromosomes), genomic DNA (in solution or bound to a solid support such as for Southern analysis), RNA (in solution or bound to  
10 a solid support such as for northern analysis), cDNA (in solution or bound to a solid support), an extract from cells or a tissue, and the like.

The term "correlates with expression of a polynucleotide", as used herein, indicates that the detection of the presence of ribonucleic acid that is similar to SEQ ID NO:2 or SEQ ID NO:4 by northern analysis is indicative of the presence of mRNA encoding UCSP in a sample and  
15 thereby correlates with expression of the transcript from the polynucleotide encoding the protein.

"Alterations" in the polynucleotide of SEQ ID NO: 2 or SEQ ID NO:4, as used herein, comprise any alteration in the sequence of polynucleotides encoding UCSP including deletions, insertions, and point mutations that may be detected using hybridization assays. Included within this definition is the detection of alterations to the genomic DNA sequence which encodes UCSP  
20 (e.g., by alterations in the pattern of restriction fragment length polymorphisms capable of hybridizing to SEQ ID NO:2 or SEQ ID NO:4), the inability of a selected fragment of SEQ ID NO: 2 or SEQ ID NO:4 to hybridize to a sample of genomic DNA (e.g., using allele-specific oligonucleotide probes), and improper or unexpected hybridization, such as hybridization to a locus other than the normal chromosomal locus for the polynucleotide sequence encoding UCSP  
25 (e.g., using fluorescent in situ hybridization [FISH] to metaphase chromosomes spreads).

As used herein, the term "antibody" refers to intact molecules as well as fragments thereof, such as Fa, F(ab')<sub>2</sub>, and Fv, which are capable of binding the epitopic determinant. Antibodies that bind UCSP polypeptides can be prepared using intact polypeptides or fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used  
30 to immunize an animal can be derived from the transition of RNA or synthesized chemically, and can be conjugated to a carrier protein, if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin and thyroglobulin. The coupled peptide is then used to immunize the animal (e.g., a mouse, a rat, or a rabbit).

The term "humanized antibody", as used herein, refers to antibody molecules in which amino acids have been replaced in the non-antigen binding regions in order to more closely resemble a human antibody, while still retaining the original binding ability.

#### THE INVENTION

5           The invention is based on the discovery of new human ubiquitin conjugation system proteins (UCSP), the polynucleotides encoding UCSP, and the use of these compositions for the diagnosis, prevention, or treatment of cancer, immune disorders, smooth muscle disorders, and viral infections.

          Nucleic acids encoding the human UCSP-1 of the present invention were first identified  
10 in Incyte Clone 2029018 from the epidermal breast keratinocyte cDNA library (KERANOT02) through a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:2, was derived from the following overlapping and/or extended nucleic acid sequences: Incyte Clones 429101/ BLADNOT01, 1684744/ PROSNOT15, 1426101/ BEPINON01, 2029018/ KERANOT02, and 2047078/THP1T7T01.

15           In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:1 as shown in Figures 1A, 1B and 1C. UCSP-1 is 259 amino acids in length and has several potential protein kinase phosphorylation sites. Potential casein kinase II phosphorylation sites are located at T54 and S96 of UCSP-1. Potential protein kinase C phosphorylation sites are located at S5, S6, T14, T138, S178, and T248. Potential tyrosine kinase  
20 phosphorylation sites are located at Y21 and Y56. Cysteine residues located at C33, C89, C94, and C157 represent potential disulfide bridging sites. As shown in Figures 3A and 3B, UCSP has chemical and structural homology with UBC6 from S. cerevisiae (GI 395781; SEQ ID NO:5) and S. pombe (GI 971980; SEQ ID NO:6). In particular, UCSP-1 shares 43% and 40% identity with UBC6 from S. cerevisiae and S. pombe, respectively. UCSP-1 shares several features common to  
25 UBC enzymes. C94 in UCSP-1 is the active cysteine residue centrally located in the UBC domain of all UBC enzymes that is necessary for thiolester formation with Ub. It is conserved in both the S. cerevisiae and S. pombe UBC6. The region surrounding this active center is also highly conserved in the three proteins. The proline-rich element N-terminal to the active cysteine residue is seen in UCSP-between approximately residues P66 and P83. The potential casein  
30 kinase II phosphorylation sites in UCSP-1 are shared by the S. pombe UBC6, as is the potential protein kinase C phosphorylation site at T138. As illustrated by Figures 5A, 5B, and 5C, UCSP and the S. cerevisiae and S. pombe UBC6 proteins have rather similar hydrophobicity plots. In particular, a prominent peak of hydrophobicity is evident at the N-terminal end of all three

proteins that corresponds to the signal-anchor sequence of UBC6. Northern analysis shows the expression of UCSP-1 in various libraries, 50% of which are associated with cancer and immortalized cell lines and 33% of which are associated with smooth muscle and the sympathetic nervous system.

5 Nucleic acids encoding the human UCSP-2 of the present invention were first identified in Incyte Clone 2151473 from the fetal brain cDNA library (BRAINOT09) through a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:2, was derived from the following overlapping and/or extended nucleic acid sequences: Incyte Clones 2606447/LUNGTUT07, 375303/LUNGNOT02, and 2151473/BRAINOT09.

10 In another embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:3 as shown in Figures 2A, 2B, 2C, and 2D. UCSP-2 is 208 amino acids in length and has potential N-linked glycosylation sites at N6, N42, N92, and N180. Cysteine residues located at C14, C18, C30, C37, C149, C152, C163, C165, C170, and C181 represent potential disulfide bridging sites. Several potential casein kinase II phosphorylation  
15 sites are located at S57, S70, S76, S103, T108, S123, and T159. As shown in Figures 4A and 4B, UCSP-2 shares chemical and structural homology with ubiquitin-like CEPs from *C. elegans* (GI 1279278; SEQ ID NO:7), and cow (GI 998680; SEQ ID NO:8). In particular, UCSP-2 shares 40% and 80% identity with the *C. elegans* and cow CEPs. UCSP-2 and the two CEPs are highly basic in their C-terminal regions where they share the highest degree of homology. The  
20 isoelectric point (pI) for UCSP-2 beginning at approximately residue 121 and extending to the C-terminus is 9.22. The corresponding values for the *C. elegans* and cow CEPs are 9.05 and 9.13, respectively. All of the cysteine residues in UCSP-2 with the exception of C66 are shared by the *C. elegans* CEP. In particular, the conservation and spacing of cysteine and histidine residues in the C-terminal region between C163 and C181 suggests a potential zinc finger, nucleic acid-  
25 binding domain. As shown in Figures 6A and 6B, UCSP-2 and *C. elegans* CEP have rather similar hydrophobicity plots. Northern analysis shows the expression of UCSP-2 in various libraries, 46% of which are associated with cancer and immortalized cell lines and 13% of which are associated with inflammation and the immune response.

The invention also encompasses UCSP variants. A preferred UCSP variant is one having  
30 at least 80%, and more preferably 90%, amino acid sequence identity to the UCSP amino acid sequence (SEQ ID NO:1 or SEQ IS NO:3). A most preferred UCSP variant is one having at least 95% amino acid sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

The invention also encompasses polynucleotide which encode UCSP. Accordingly, any

nucleic acid sequence which encodes the amino acid sequence of UCSP can be used to generate recombinant molecules which express UCSP. In a particular embodiment, the invention encompasses the polynucleotide comprising the nucleic acid sequence of SEQ ID NO:2 or SEQ ID NO:4 as shown in Figures 1A, 1B, 1C or Figures 3A and 3B, respectively.

5 It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of nucleotide sequences encoding UCSP, some bearing minimal homology to the nucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These  
10 combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence of naturally occurring UCSP, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode UCSP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring UCSP under  
15 appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding UCSP or its derivatives possessing a substantially different codon usage. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence  
20 encoding UCSP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences, or portions thereof, which encode UCSP and its derivatives, entirely by synthetic chemistry. After production, the  
25 synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art at the time of the filing of this application. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding UCSP or any portion thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of  
30 hybridizing to the claimed nucleotide sequences, and in particular, those shown in SEQ ID NO:2 and SEQ ID NO:4, under various conditions of stringency. Hybridization conditions are based on the melting temperature ( $T_m$ ) of the nucleic acid binding complex or probe, as taught in Wahl, G.M. and S.L. Berger (1987; Methods Enzymol. 152:399-407) and Kimmel, A.R. (1987;

Methods Enzymol. 152:507-511), and may be used at a defined stringency.

Altered nucleic acid sequences encoding UCSP which are encompassed by the invention include deletions, insertions, or substitutions of different nucleotides resulting in a polynucleotide that encodes the same or a functionally equivalent UCSP. The encoded protein may also contain  
5 deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent UCSP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the biological activity of UCSP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid; positively  
10 charged amino acids may include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; phenylalanine and tyrosine.

Also included within the scope of the present invention are alleles of the genes encoding UCSP. As used herein, an "allele" or "allelic sequence" is an alternative form of the gene which  
15 may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times  
20 in a given sequence.

Methods for DNA sequencing which are well known and generally available in the art may be used to practice any embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, Sequenase® (US Biochemical Corp, Cleveland, OH), Taq polymerase (Perkin Elmer), thermostable T7 polymerase (Amersham,  
25 Chicago, IL), or combinations of recombinant polymerases and proofreading exonucleases such as the ELONGASE Amplification System marketed by Gibco BRL (Gaithersburg, MD). Preferably, the process is automated with machines such as the Hamilton Micro Lab 2200 (Hamilton, Reno, NV), Peltier Thermal Cycler (PTC200; MJ Research, Watertown, MA) and the ABI 377 DNA sequencers (Perkin Elmer).

30 The nucleic acid sequences encoding UCSP may be extended utilizing a partial nucleotide sequence and employing various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, one method which may be employed, "restriction-site" PCR, uses universal primers to retrieve unknown sequence adjacent to a known

locus (Sarkar, G. (1993) PCR Methods Applic. 2:318-322). In particular, genomic DNA is first amplified in the presence of primer to linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are  
5 transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR may also be used to amplify or extend sequences using divergent primers based on a known region (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). The primers may be designed using OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, MN), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of  
10 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Another method which may be used is capture PCR which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA  
15 (Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119). In this method, multiple restriction enzyme digestions and ligations may also be used to place an engineered double-stranded sequence into an unknown portion of the DNA molecule before performing PCR.

Another method which may be used to retrieve unknown sequences is that of Parker, J.D.  
20 et al. (1991; Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PromoterFinder™ libraries to walk in genomic DNA (Clontech, Palo Alto, CA). This process avoids the need to screen libraries and is useful in finding intron/exon junctions. When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Also, random-primed libraries are preferable, in that they  
25 will contain more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into the 5' and 3' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to  
30 analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity may be



converted to electrical signal using appropriate software (e.g. Genotyper™ and Sequence Navigator™, Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts  
5 in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode UCSP, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of UCSP in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the  
10 same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express UCSP.

As will be understood by those of skill in the art, it may be advantageous to produce UCSP-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate  
15 of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter UCSP encoding sequences for a variety of reasons,  
20 including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

25 In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding UCSP may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of UCSP activity, it may be useful to encode a chimeric UCSP protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the UCSP  
30 encoding sequence and the heterologous protein sequence, so that UCSP may be cleaved and purified away from the heterologous moiety.

In another embodiment, sequences encoding UCSP may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M.H. et al. (1980) Nucl.

Acids Res. Symp. Ser. 215-223, Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of UCSP, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J.Y. et al. (1995) Science 269:202-204) and  
5 automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer).

The newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, NY). The composition of the synthetic  
10 peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; Creighton, supra). Additionally, the amino acid sequence of UCSP, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a biologically active UCSP, the nucleotide sequences encoding UCSP  
15 or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence.

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding UCSP and appropriate transcriptional and  
20 translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, NY, and Ausubel, F.M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY.

25 A variety of expression vector/host systems may be utilized to contain and express sequences encoding UCSP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression  
30 vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular

proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid  
5 lacZ promoter of the Bluescript® phagemid (Stratagene, LaJolla, CA) or pSport1™ plasmid (Gibco BRL) and the like may be used. The baculovirus polyhedrin promoter may be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (e.g., heat shock, RUBISCO; and storage protein genes) or from plant viruses (e.g., viral promoters or leader sequences) may be cloned into the vector. In mammalian cell systems, promoters from  
10 mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding UCSP, vectors based on SV40 or EBV may be used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for UCSP. For example, when large quantities of UCSP are needed for the  
15 induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional E. coli cloning and expression vectors such as Bluescript® (Stratagene), in which the sequence encoding UCSP may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of  $\beta$ -galactosidase so that a hybrid protein is produced; pIN  
20 vectors (Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors (Promega, Madison, WI) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to  
25 include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, Saccharomyces cerevisiae, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) Methods Enzymol. 153:516-544.

30 In cases where plant expression vectors are used, the expression of sequences encoding UCSP may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant

promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection.

- 5 Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L.E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, NY; pp. 191-196.

An insect system may also be used to express UCSP. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign  
10 genes in Spodoptera frugiperda cells or in Trichoplusia larvae. The sequences encoding UCSP may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of UCSP will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, S. frugiperda cells or Trichoplusia larvae in  
15 which UCSP may be expressed (Engelhard, E.K. et al. (1994) Proc. Nat. Acad. Sci. 91:3224-3227).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding UCSP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and  
20 tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing UCSP in infected host cells (Logan, J. and Shenk, T. (1984) Proc. Natl. Acad. Sci. 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

25 Specific initiation signals may also be used to achieve more efficient translation of sequences encoding UCSP. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding UCSP, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a  
30 portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may

be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express UCSP may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1980) *Cell* 22:817-23) genes which can be employed in tk<sup>-</sup> or apt<sup>-</sup> cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14) and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, supra). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S.C. and R.C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). Recently, the use of visible markers has gained popularity with such markers as anthocyanins,  $\beta$  glucuronidase and its substrate GUS, and

luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding UCSP is inserted within a marker gene sequence, recombinant cells containing sequences encoding UCSP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding UCSP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells which contain the nucleic acid sequence encoding UCSP and express UCSP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

The presence of polynucleotide sequences encoding UCSP can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or portions or fragments of polynucleotides encoding UCSP. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the sequences encoding UCSP to detect transformants containing DNA or RNA encoding UCSP. As used herein "oligonucleotides" or "oligomers" refer to a nucleic acid sequence of at least about 10 nucleotides and as many as about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20-25 nucleotides, which can be used as a probe or amplifier.

A variety of protocols for detecting and measuring the expression of UCSP, using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on UCSP is preferred, but a competitive binding assay may be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul, MN) and Maddox, D.E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled

hybridization or PCR probes for detecting sequences related to polynucleotides encoding UCSP include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding UCSP, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are  
5 commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits (Pharmacia & Upjohn, (Kalamazoo, MI); Promega (Madison WI); and U.S. Biochemical Corp., Cleveland, OH). Suitable reporter molecules or labels, which may be used, include radionuclides, enzymes,  
10 fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding UCSP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the  
15 sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode UCSP may be designed to contain signal sequences which direct secretion of UCSP through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding UCSP to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins.  
20 Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, WA). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San  
25 Diego, CA) between the purification domain and UCSP may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing UCSP and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3:263-281) while the  
30 enterokinase cleavage site provides a means for purifying UCSP from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D.J. et al. (1993; DNA Cell Biol. 12:441-453).

In addition to recombinant production, fragments of UCSP may be produced by direct

peptide synthesis using solid-phase techniques Merrifield J. (1963) J. Am. Chem. Soc. 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Various fragments of UCSP may be chemically synthesized  
5 separately and combined using chemical methods to produce the full length molecule.

## THERAPEUTICS

Chemical and structural homology exists among UCSP-1 and UBC6 from S. cerevisiae and S.pombe. In addition, northern analysis shows the expression of UCSP-1 in tissues associated with cancer and smooth muscle. UCSP therefore appears to be associated with the  
10 development of cancer and smooth muscle disorders. In addition, the known function of the UCS in processing viral proteins implicates UCSP-1 in the development of viral diseases.

The UCS is involved in the degradation of certain oncogenic proteins. Therefore a decrease in the level or activity of UCSP-1 appears to be associated with the development of cancer. Therefore in one embodiment, UCSP-1 or a fragment or derivative thereof, may be  
15 administered to a subject to treat or prevent cancer, including astrocytoma, glioma, ganglioneuroma, neurocytoma, neuroblastoma, adenocarcinoma, sarcoma, melanoma, lymphoma, leukemia, and myeloma. In particular, types of cancer may include, but are not limited to, cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis,  
20 prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing UCSP-1, or a fragment or a derivative thereof, may also be administered to a subject to treat or prevent any of the types of cancer listed above.

A decrease in the level or activity of UCSP-1 also appears to be associated with the  
25 development of smooth muscle disorders. Therefore in another embodiment, UCSP-1 or a fragment or derivative thereof, may be administered to a subject to treat or prevent a smooth muscle disorder. A smooth muscle disorder is defined as any impairment or alteration in the normal action of smooth muscle and may include, but is not limited to, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension,  
30 hypoglycemia, myocardial infarction, migraine, and pheochromocytoma, and myopathies including cardiomyopathy, encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, and ophthalmoplegia. Smooth muscle is a component of the blood vessels, gastrointestinal tract, heart, and uterus.



In another embodiment, a vector capable of expressing UCSP-1, or a fragment or a derivative thereof, may also be administered to a subject to treat or prevent any of the smooth muscle disorders listed above.

An increase in the level or activity of UCSP-1 appears to be associated with the development of viral diseases. Therefore in another embodiment, an antagonist or inhibitor of UCSP-1 may be administered to a subject to treat or prevent viral diseases. Viral diseases may include, but are not limited to, adenoviruses (ARD, pneumonia), arenaviruses (lymphocytic choriomeningitis), bunyaviruses (Hantavirus), coronaviruses (pneumonia, chronic bronchitis), hepadnaviruses (hepatitis), herpesviruses (HSV, VZV, Epstein-Barr virus, cytomegalovirus), flaviviruses (yellow fever), orthomyxoviruses (influenza), papillomaviruses (cancer), paramyxoviruses (measles, mumps), picornoviruses (rhinovirus, poliovirus, coxsackie-virus), polyomaviruses (BK virus, JC virus), poxviruses (smallpox), reovirus (Colorado tick fever), retroviruses (HIV, HTLV), rhabdoviruses (rabies), rotaviruses (gastroenteritis), and togaviruses (encephalitis, rubella,). In one aspect of this embodiment, antibodies which are specific for UCSP-1 may be used directly as an antagonist, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express UCSP-1.

In another embodiment, the complement of the polynucleotide encoding UCSP-1 or an antisense molecule may be administered to a subject to treat or prevent any of the viral diseases listed above.

Chemical and structural homology exists among UCSP-2 and ubiquitin-like CEP proteins from Caenorhabditis elegans and cow. In addition, northern analysis shows the expression of UCSP-2 in tissues associated with cancer and the immune system. UCSP-2 therefore appears to be associated with the development of cancer and immune disorders.

A decrease in the level or activity of UCSP-2 appears to be associated with the development of cancer. Therefore in another embodiment, UCSP-2, or a fragment or derivative thereof, may be administered to a subject to treat or prevent cancer, including astrocytoma, glioma, ganglioneuroma, neurocytoma, neuroblastoma, adenocarcinoma, sarcoma, melanoma, lymphoma, leukemia, and myeloma. In particular, types of cancer may include, but are not limited to, cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing UCSP-2, or a fragment or a derivative thereof, may also be administered to a subject to treat or prevent any of the types of

cancer listed above.

An increase in the level or activity of UCSP-2 appears to be associated with the development of immune disorders. Therefore in another embodiment, an antagonist or inhibitor of UCSP-2 may be administered to a subject to treat or prevent an immune disorder. Such disorders may include, but are not limited to, AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anemia, asthma, atherosclerosis, bronchitis, cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis, gout, Graves' disease, hypereosinophilia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjögren's syndrome, and autoimmune thyroiditis; complications of cancer, hemodialysis, extracorporeal circulation; viral, bacterial, fungal, parasitic, protozoal, and helminthic infections and trauma. In one aspect of this embodiment, antibodies which are specific for UCSP-2 may be used directly as an antagonist, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express UCSP-2.

In another embodiment, the complement of the polynucleotide encoding UCSP-2 or an antisense molecule may be administered to a subject to treat or prevent any of the immune disorders listed above.

In other embodiments, any of the therapeutic proteins, antagonists, antibodies, agonists, antisense sequences or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

Antagonists or inhibitors of UCSP may be produced using methods which are generally known in the art. In particular, purified UCSP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind UCSP.

The antibodies may be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies, (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others, may be immunized by injection with UCSP or any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the peptides, fragments, or oligopeptides used to induce antibodies to UCSP have an amino acid sequence consisting of at least five amino acids, and more preferably at least 10 amino acids. It is also preferable that they are identical to a portion of the amino acid sequence of the natural protein, and they may contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of UCSP amino acids may be fused with those of another protein such as keyhole limpet hemocyanin and antibody produced against the chimeric molecule.

Monoclonal antibodies to UCSP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. 80:2026-2030; Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120).

In addition, techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can be used (Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; Takeda, S. et al. (1985) Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce UCSP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries (Burton D.R. (1991) Proc. Natl. Acad. Sci. 88:11120-3).

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86:

3833-3837; Winter, G. et al. (1991) Nature 349:293-299).

Antibody fragments which contain specific binding sites for UCSP may also be generated. For example, such fragments include, but are not limited to, the F(ab')<sub>2</sub> fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be  
5 generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse, W.D. et al. (1989) Science 254:1275-1281).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays  
10 using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between UCSP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering UCSP epitopes is preferred, but a competitive binding assay may also be employed (Maddox, supra).

15 In another embodiment of the invention, the polynucleotides encoding UCSP, or any fragment thereof, or antisense molecules, may be used for therapeutic purposes. In one aspect, antisense to the polynucleotide encoding UCSP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding UCSP. Thus, antisense molecules may be  
20 used to modulate UCSP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligomers or larger fragments, can be designed from various locations along the coding or control regions of sequences encoding UCSP.

Expression vectors derived from retro viruses, adenovirus, herpes or vaccinia viruses, or from various bacterial plasmids may be used for delivery of nucleotide sequences to the targeted  
25 organ, tissue or cell population. Methods which are well known to those skilled in the art can be used to construct recombinant vectors which will express antisense molecules complementary to the polynucleotides of the gene encoding UCSP. These techniques are described both in Sambrook et al. (supra) and in Ausubel et al. (supra).

Genes encoding UCSP can be turned off by transforming a cell or tissue with expression  
30 vectors which express high levels of a polynucleotide or fragment thereof which encodes UCSP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a

month or more with a non-replicating vector and even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing antisense molecules, DNA, RNA, or PNA, to the control regions of the gene encoding UCSP, i.e.,  
5 the promoters, enhancers, and introns. Oligonucleotides derived from the transcription initiation site, e.g., between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using  
10 triplex DNA have been described in the literature (Gee, J.E. et al. (1994) In: Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, NY). The antisense molecules may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage  
15 of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Examples which may be used include engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding UCSP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified  
20 by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with  
25 complementary oligonucleotides using ribonuclease protection assays.

Antisense molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription  
30 of DNA sequences encoding UCSP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize antisense RNA constitutively or inducibly can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of  
5 PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally  
10 suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection and by liposome injections may be achieved using methods which are well known in the art.

Any of the therapeutic methods described above may be applied to any subject in need of  
15 such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

An additional embodiment of the invention relates to the administration of a pharmaceutical composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of  
20 UCSP, antibodies to UCSP, mimetics, agonists, antagonists, or inhibitors of UCSP. The compositions may be administered alone or in combination with at least one other agent, such as stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs  
25 or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

30 In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found

in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton, PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles

include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

5 For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

10 The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and  
15 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of UCSP, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions  
20 wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models, usually mice, rabbits, dogs, or  
25 pigs. The animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example UCSP or fragments thereof, antibodies of UCSP, agonists, antagonists or inhibitors of UCSP,  
30 which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ED50 (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic



index, and it can be expressed as the ratio, LD50/ED50. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the  
5 ED50 with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into  
10 account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular formulation.

15 Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to  
20 particular cells, conditions, locations, etc.

## DIAGNOSTICS

In another embodiment, antibodies which specifically bind UCSP may be used for the diagnosis of conditions or diseases characterized by expression of UCSP, or in assays to monitor patients being treated with UCSP, agonists, antagonists or inhibitors. The antibodies useful for  
25 diagnostic purposes may be prepared in the same manner as those described above for therapeutics. Diagnostic assays for UCSP include methods which utilize the antibody and a label to detect UCSP in human body fluids or extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule. A wide variety of reporter molecules which are known  
30 in the art may be used, several of which are described above.

A variety of protocols including ELISA, RIA, and FACS for measuring UCSP are known in the art and provide a basis for diagnosing altered or abnormal levels of UCSP expression. Normal or standard values for UCSP expression are established by combining body fluids or cell

extracts taken from normal mammalian subjects, preferably human, with antibody to UCSP under conditions suitable for complex formation. The amount of standard complex formation may be quantified by various methods, but preferably by photometric, means. Quantities of UCSP expressed in subject, control and disease, samples from biopsied tissues are compared with the  
5 standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding UCSP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, antisense RNA and DNA molecules, and PNAs. The polynucleotides may be used to  
10 detect and quantitate gene expression in biopsied tissues in which expression of UCSP may be correlated with disease. The diagnostic assay may be used to distinguish between absence, presence, and excess expression of UCSP, and to monitor regulation of UCSP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting  
15 polynucleotide sequences, including genomic sequences, encoding UCSP or closely related molecules, may be used to identify nucleic acid sequences which encode UCSP. The specificity of the probe, whether it is made from a highly specific region, e.g., 10 unique nucleotides in the 5' regulatory region, or a less specific region, e.g., especially in the 3' coding region, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low) will  
20 determine whether the probe identifies only naturally occurring sequences encoding UCSP, alleles, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably contain at least 50% of the nucleotides from any of the UCSP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and derived from the  
25 nucleotide sequence of SEQ ID NO:2 or from genomic sequence including promoter, enhancer elements, and introns of the naturally occurring UCSP.

Means for producing specific hybridization probes for DNAs encoding UCSP include the cloning of nucleic acid sequences encoding UCSP or UCSP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, commercially available, and  
30 may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, radionuclides such as <sup>32</sup>P or <sup>35</sup>S, or enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the

like.

Polynucleotide sequences encoding UCSP may be used for the diagnosis of conditions or diseases which are associated with expression of UCSP. Examples of such conditions or diseases include cancer such as cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; smooth muscle disorders such as angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, and pheochromocytoma, and myopathies including cardiomyopathy, encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, and ophthalmoplegia; viral diseases such as adenoviruses (ARD, pneumonia), arenaviruses (lymphocytic choriomeningitis), bunyaviruses (Hantavirus), coronaviruses (pneumonia, chronic bronchitis), hepadnaviruses (hepatitis), herpesviruses (HSV, VZV, Epstein-Barr virus, cytomegalovirus), flaviviruses (yellow fever), orthomyxoviruses (influenza), papillomaviruses (cancer), paramyxoviruses (measles, mumps), picornaviruses (rhinovirus, poliovirus, coxsackie-virus), polyomaviruses (BK virus, JC virus), poxviruses (smallpox), reovirus (Colorado tick fever), retroviruses (HIV, HTLV), rhabdoviruses (rabies), rotaviruses (gastroenteritis), and togaviruses (encephalitis, rubella); and immune disorders such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anemia, asthma, atherosclerosis, bronchitis, cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis, gout, Graves' disease, hypereosinophilia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjögren's syndrome, and autoimmune thyroiditis; complications of cancer, hemodialysis, extracorporeal circulation; viral, bacterial, fungal, parasitic, protozoal, and helminthic infections and trauma. The polynucleotide sequences encoding UCSP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; or in dip stick, pin, ELISA or chip assays utilizing fluids or tissues from patient biopsies to detect altered UCSP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding UCSP may be useful in assays that detect activation or induction of various cancers, particularly those mentioned above. The nucleotide sequences encoding UCSP may be labeled by standard methods, and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization

complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the biopsied or extracted sample is significantly altered from that of a comparable control sample, the nucleotide sequences have hybridized with nucleotide sequences in the sample, and the presence of altered levels of  
5 nucleotide sequences encoding UCSP in the sample indicates the presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or in monitoring the treatment of an individual patient.

In order to provide a basis for the diagnosis of disease associated with expression of  
10 UCSP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, which encodes UCSP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with those from an experiment where a known amount of a  
15 substantially purified polynucleotide is used. Standard values obtained from normal samples may be compared with values obtained from samples from patients who are symptomatic for disease. Deviation between standard and subject values is used to establish the presence of disease.

Once disease is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to evaluate whether the level of expression in the patient begins to  
20 approximate that which is observed in the normal patient. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or  
25 may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding  
30 UCSP may involve the use of PCR. Such oligomers may be chemically synthesized, generated enzymatically, or produced from a recombinant source. Oligomers will preferably consist of two nucleotide sequences, one with sense orientation (5'→3') and another with antisense (3'←5'), employed under optimized conditions for identification of a specific gene or condition. The same

two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of UCSP include  
5 radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated (Melby, P.C. et al. (1993) J. Immunol. Methods, 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 229-236). The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or  
10 colorimetric response gives rapid quantitation.

In another embodiment of the invention, the nucleic acid sequences which encode UCSP may also be used to generate hybridization probes which are useful for mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome or to a specific region of the chromosome using well known techniques. Such techniques include FISH,  
15 FACS, or artificial chromosome constructions, such as yeast artificial chromosomes, bacterial artificial chromosomes, bacterial P1 constructions or single chromosome cDNA libraries as reviewed in Price, C.M. (1993) Blood Rev. 7:127-134, and Trask, B.J. (1991) Trends Genet. 7:149-154.

FISH (as described in Verma et al. (1988) Human Chromosomes: A Manual of Basic  
20 Techniques, Pergamon Press, New York, NY) may be correlated with other physical chromosome mapping techniques and genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of the gene encoding UCSP on a physical chromosomal map and a specific disease, or predisposition to a specific disease, may help delimit the region of DNA associated with that genetic disease. The  
25 nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier, or affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as  
30 mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms, or parts thereof, by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or

syndrome has been crudely localized by genetic linkage to a particular genomic region, for example, AT to 11q22-23 (Gatti, R.A. et al. (1988) Nature 336:577-580), any sequences mapping to that area may represent associated or regulatory genes for further investigation. The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier, or affected individuals.

In another embodiment of the invention, UCSP, its catalytic or immunogenic fragments or oligopeptides thereof, can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes, between UCSP and the agent being tested, may be measured.

Another technique for drug screening which may be used provides for high throughput screening of compounds having suitable binding affinity to the protein of interest as described in published PCT application WO84/03564. In this method, as applied to UCSP large numbers of different small test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with UCSP, or fragments thereof, and washed. Bound UCSP is then detected by methods well known in the art. Purified UCSP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding UCSP specifically compete with a test compound for binding UCSP. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with UCSP.

In additional embodiments, the nucleotide sequences which encode UCSP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

The examples below are provided to illustrate the subject invention and are not included for the purpose of limiting the invention.

## **INDUSTRIAL APPLICABILITY**

### **I KERANOT02 cDNA Library Construction**

The KERANOT02 cDNA library was constructed from cryopreserved normal epidermal keratinocytes purchased from Clonetics (San Diego, CA). The tissue donor was a 30 year old

Afro-American female whose skin was resected during elective breast reduction surgery. At the time of surgery, the donor was taking ferrous sulfate in preparation for the surgery, and a routine blood test was unremarkable except for a slight elevation of serum alanine transferase.

One ampule of  $7.6 \times 10^5$  cells was cultured and expanded in media and supplements  
5 provided by Clonetics, following the recommended protocol, except that use of bovine pituitary extract was omitted. After a single passage,  $3 \times 10^7$  cells were harvested and lysed using a Brinkmann Homogenizer Polytron PT-3000 (Brinkmann Instruments, Westbury NJ) in guanidinium isothiocyanate solution. The lysate was centrifuged over a 5.7 M CsCl cushion using an Beckman SW28 rotor in a Beckman L8-70M Ultracentrifuge (Beckman Instruments) for  
10 18 hours at 25,000 rpm at ambient temperature. The RNA was extracted with phenol chloroform pH 8.0, precipitated using 0.3 M sodium acetate and 2.5 volumes of ethanol, resuspended in RNase-free water and DNase treated at 37°C. RNA extraction and precipitation was repeated as before. The mRNA was then isolated using the Qiagen Oligotex kit (QIAGEN Inc; Chatsworth, CA) and used to construct the cDNA library.

15 The mRNA was handled according to the recommended protocols in the SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning (Cat. #18248-013; Gibco/BRL, Gaithersburg, MD). cDNAs were fractionated on a Sepharose CL4B column (Cat. #275105-01; Pharmacia), and those cDNAs exceeding 400 bp were ligated into pSport I. The plasmid pSport I was subsequently transformed into DH5a™ competent cells (Cat. #18258-012; Gibco/BRL).

## 20 II BRAINOT09 cDNA Library Construction

The BRAINOT09 cDNA library was constructed from fetal brain tissue obtained from a 25-week-old Caucasian male (International Institute of Advanced Medicine, Exton, PA) who was delivered after 25 week gestation and died soon thereafter. Family history included diabetes in the mother.

25 The frozen tissue was homogenized and lysed using a Brinkmann Homogenizer Polytron-PT 3000 (Brinkmann Instruments, Inc., Westbury, NY) in guanidinium isothiocyanate solution. The lysates were extracted once with acid phenol at pH 4.7 per Stratagene's RNA isolation protocol (Stratagene, Inc.). The RNA was extracted once with an equal volume of acid phenol, reprecipitated using 0.3 M sodium acetate and 2.5 volumes of ethanol, resuspended in  
30 DEPC-treated water and DNase treated for 25 min at 37°C. mRNAs were isolated using the Qiagen Oligotex kit (QIAGEN, Inc.; Chatworth, CA) and used to construct the cDNA library.

The mRNA was handled according to the recommended protocols in the SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning (Cat. #18248-013; Gibco/BRL).

cDNAs were fractionated on a Sepharose CL4B column (Cat. #275105-01; Pharmacia), and those cDNAs exceeding 400 bp were ligated into pSport I. The plasmid pSport I was subsequently transformed into DH5a<sup>TM</sup> competent cells (Cat. #18258-012; Gibco/BRL).

### III Isolation and Sequencing of cDNA Clones

5 Plasmid DNA was released from the cells and purified using the REAL Prep 96 Plasmid Kit (Catalog #26173; QIAGEN Inc). This kit enables the simultaneous purification of 96 samples in a 96-well block using multi-channel reagent dispensers. The recommended protocol was employed except for the following changes: 1) the bacteria were cultured in 1 ml of sterile Terrific Broth (Catalog #22711, Gibco/BRL) with carbenicillin at 25 mg/L and glycerol at 0.4%;  
10 2) the cultures were incubated for 19 hours after the wells were inoculated and then lysed with 0.3 ml of lysis buffer; 3) following isopropanol precipitation, the plasmid DNA pellet was resuspended in 0.1 ml of distilled water. After the last step in the protocol, samples were transferred to a Beckman 96-well block for storage.

The cDNAs were sequenced by the method of Sanger F and AR Coulson (1975; J Mol  
15 Biol 94:441f), using a Hamilton Micro Lab 2200 (Hamilton, Reno NV) in combination with Peltier Thermal Cyclers (PTC200 from MJ Research, Watertown MA) and Applied Biosystems 377 or 373 DNA Sequencing Systems; and the reading frame was determined.

### IV Homology Searching of cDNA Clones and Their Deduced Proteins

The nucleotide sequences of the Sequence Listing or amino acid sequences deduced from  
20 them were used as query sequences against databases such as GenBank, SwissProt, BLOCKS, and Pima II. These databases which contain previously identified and annotated sequences were searched for regions of homology (similarity) using BLAST, which stands for Basic Local Alignment Search Tool (Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul et al. (1990) J. Mol. Biol. 215:403-410).

25 BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches or in identifying homologs which may be of prokaryotic (bacterial) or eukaryotic (animal, fungal or plant) origin. Other algorithms such as the one described in Smith RF and TF Smith (1992; Protein Engineering 5:35-51), incorporated herein by reference, can be  
30 used when dealing with primary sequence patterns and secondary structure gap penalties. As disclosed in this application, the sequences have lengths of at least 49 nucleotides, and no more than 12% uncalled bases (where N is recorded rather than A, C, G, or T).

The BLAST approach, as detailed in Karlin, S. and S.F. Atschul (1993; Proc. Nat. Acad.



Sci. 90:5873-7) and incorporated herein by reference, searches for matches between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. In this application, threshold was set at  $10^{-25}$  for nucleotides and  $10^{-14}$  for peptides.

5 Incyte nucleotide sequences were searched against the GenBank databases for primate (pri), rodent (rod), and mammalian sequences (mam), and deduced amino acid sequences from the same clones are searched against GenBank functional protein databases, mammalian (mamp), vertebrate (vrtp) and eukaryote (eukp), for homology. The relevant database for a particular match were reported as a Gxxxx±p (where xxx is pri, rod, etc and if present, p = peptide).

## 10 V Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound (Sambrook et al., supra).

Analogous computer techniques using BLAST (Altschul, S.F. 1993 and 1990, supra) are  
15 used to search for identical or related molecules in nucleotide databases such as GenBank or the LIFESEQ™ database (Incyte Pharmaceuticals). This analysis is much faster than multiple, membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or homologous.

The basis of the search is the product score which is defined as:

$$20 \quad \frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1-2% error; and at 70, the match will be exact. Homologous molecules are usually  
25 identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analysis are reported as a list of libraries in which the transcript encoding UCSP occurs. Abundance and percent abundance are also reported. Abundance directly reflects the number of times a particular transcript is represented in a cDNA library, and  
30 percent abundance is abundance divided by the total number of sequences examined in the cDNA library.

## VI Extension of UCSP-Encoding Polynucleotides

Nucleic acid sequence of Incyte Clone 2029018 or 2151473, or SEQ ID NO:2 or SEQ ID

NO:4, respectively, is used to design oligonucleotide primers for extending a partial nucleotide sequence to full length or for obtaining 5' or 3', intron or other control sequences from genomic libraries. One primer is synthesized to initiate extension in the antisense direction (XLR) and the other is synthesized to extend sequence in the sense direction (XLF). Primers are used to  
 5 facilitate the extension of the known sequence "outward" generating amplicons containing new, unknown nucleotide sequence for the region of interest. The initial primers are designed from the cDNA using OLIGO 4.06 (National Biosciences), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. Any stretch of nucleotides which would result in hairpin  
 10 structures and primer-primer dimerizations is avoided.

The original, selected cDNA libraries, or a human genomic library are used to extend the sequence; the latter is most useful to obtain 5' upstream regions. If more extension is necessary or desired, additional sets of primers are designed to further extend the known region.

By following the instructions for the XL-PCR kit (Perkin Elmer) and thoroughly mixing  
 15 the enzyme and reaction mix, high fidelity amplification is obtained. Beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, PCR is performed using the Peltier Thermal Cycler (PTC200; M.J. Research, Watertown, MA) and the following parameters:

20	Step 1	94° C for 1 min (initial denaturation)
	Step 2	65° C for 1 min
	Step 3	68° C for 6 min
	Step 4	94° C for 15 sec
	Step 5	65° C for 1 min
	Step 6	68° C for 7 min
25	Step 7	Repeat step 4-6 for 15 additional cycles
	Step 8	94° C for 15 sec
	Step 9	65° C for 1 min
	Step 10	68° C for 7:15 min
	Step 11	Repeat step 8-10 for 12 cycles
30	Step 12	72° C for 8 min
	Step 13	4° C (and holding)

A 5-10  $\mu$ l aliquot of the reaction mixture is analyzed by electrophoresis on a low concentration (about 0.6-0.8%) agarose mini-gel to determine which reactions were successful in  
 35 extending the sequence. Bands thought to contain the largest products are selected and removed from the gel. Further purification involves using a commercial gel extraction method such as QIAQuick™ (QIAGEN Inc., Chatsworth, CA). After recovery of the DNA, Klenow enzyme is

used to trim single-stranded, nucleotide overhangs creating blunt ends which facilitate religation and cloning.

After ethanol precipitation, the products are redissolved in 13  $\mu$ l of ligation buffer, 1  $\mu$ l T4-DNA ligase (15 units) and 1  $\mu$ l T4 polynucleotide kinase are added, and the mixture is  
5 incubated at room temperature for 2-3 hours or overnight at 16° C. Competent *E. coli* cells (in 40  $\mu$ l of appropriate media) are transformed with 3  $\mu$ l of ligation mixture and cultured in 80  $\mu$ l of SOC medium (Sambrook et al., supra). After incubation for one hour at 37° C, the whole transformation mixture is plated on Luria Bertani (LB)-agar (Sambrook et al., supra) containing 2x Carb. The following day, several colonies are randomly picked from each plate and cultured  
10 in 150  $\mu$ l of liquid LB/2x Carb medium placed in an individual well of an appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5  $\mu$ l of each overnight culture is transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5  $\mu$ l of each sample is transferred into a PCR array.

For PCR amplification, 18  $\mu$ l of concentrated PCR reaction mix (3.3x) containing 4 units  
15 of rTth DNA polymerase, a vector primer, and one or both of the gene specific primers used for the extension reaction are added to each well. Amplification is performed using the following conditions:

	Step 1	94° C for 60 sec
	Step 2	94° C for 20 sec
20	Step 3	55° C for 30 sec
	Step 4	72° C for 90 sec
	Step 5	Repeat steps 2-4 for an additional 29 cycles
	Step 6	72° C for 180 sec
	Step 7	4° C (and holding)

25 Aliquots of the PCR reactions are run on agarose gels together with molecular weight markers. The sizes of the PCR products are compared to the original partial cDNAs, and appropriate clones are selected, ligated into plasmid, and sequenced.

## VII Labeling and Use of Hybridization Probes

Hybridization probes derived from SEQ ID NO:2 or SEQ ID NO:4 are employed to  
30 screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base-pairs, is specifically described, essentially the same procedure is used with larger cDNA fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 (National Biosciences), labeled by combining 50 pmol of each oligomer and 250  $\mu$ Ci of [ $\gamma$ -<sup>32</sup>P] adenosine triphosphate (Amersham) and T4 polynucleotide kinase (DuPont NEN®,  
35 Boston, MA). The labeled oligonucleotides are substantially purified with Sephadex G-25

superfine resin column (Pharmacia & Upjohn). A portion containing  $10^7$  counts per minute of each of the sense and antisense oligonucleotides is used in a typical membrane based hybridization analysis of human genomic DNA digested with one of the following endonucleases (Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II; DuPont NEN®).

- 5 The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham, NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR™ film (Kodak, Rochester, NY) is exposed to the  
10 blots in a Phosphorimager cassette (Molecular Dynamics, Sunnyvale, CA) for several hours, hybridization patterns are compared visually.

### VIII Complementary Polynucleotide, Antisense Molecules

Polynucleotide complementary to the UCSP-encoding sequence, or any part thereof, or an antisense molecule is used to inhibit in vivo expression of naturally occurring UCSP.

- 15 Although use of antisense oligonucleotides, comprising about 20 base-pairs, is specifically described, essentially the same procedure is used with larger cDNA fragments. An oligonucleotide based on the coding sequences of UCSP, as shown in Figures 1A, 1B and 1C or Figures 2A, 2B, 2C and 2D, is used to inhibit expression of naturally occurring UCSP. The complementary oligonucleotide is designed from the most unique 5' sequence as shown in  
20 Figures 1A, 1B and 1C or Figures 2A, 2B, 2C and 2D and used either to inhibit transcription by preventing promoter binding to the upstream nontranslated sequence or translation of an UCSP-encoding transcript by preventing the ribosome from binding. Using an appropriate portion of the signal and 5' sequence of SEQ ID NO:2 or SEQ ID NO:4, an effective antisense oligonucleotide includes any 15-20 nucleotides spanning the region which translates into the  
25 signal or 5' coding sequence of the polypeptide as shown in Figures 1A, 1B and 1C or Figures 2A, 2B, 2C and 2D.

### IX Expression of UCSP

- Expression of UCSP is accomplished by subcloning the cDNAs into appropriate vectors and transforming the vectors into host cells. In this case, the cloning vector is used to express  
30 UCSP in E. coli. Upstream of the cloning site, this vector contains a promoter for  $\beta$ -galactosidase, followed by sequence containing the amino-terminal Met, and the subsequent seven residues of  $\beta$ -galactosidase. Immediately following these eight residues is a bacteriophage promoter useful for transcription and a linker containing a number of unique restriction sites.

Induction of an isolated, transformed bacterial strain with IPTG using standard methods produces a fusion protein which consists of the first eight residues of  $\beta$ -galactosidase, about 5 to 15 residues of linker, and the full length protein. The signal residues direct the secretion of UCSP into the bacterial growth media which can be used directly in the following assay for activity.

## **IX Demonstration of UCSP Activity**

### **UCSP-1**

UCSP-1 activity may be measured by the ability of UBC6 enzymes to suppress translocation of proteins in yeast cells containing a defective sec61 gene (Jentsch, supra). SEC61 protein is involved in the translocation of certain other proteins (KAR2, CPY, and a-factor) across the endoplasmic reticulum in yeast cells. In mutant yeast cells containing a defective SEC61 protein subunit (sec61 mutants), the defective protein is degraded by a UBC6 dependent pathway. This degradation results in the accumulation of unprocessed precursors of KAR2, CPY, and a-factor. Double mutants defective in both UBC6 expression and normal SEC16 protein expression (sec16/ubc6) translocate proteins normally. UCSP-1 may therefore be measured by suppression of protein translocation in sec16/ubc6 cells transfected with the gene expressing UCSP-1. Accumulation of unprocessed precursors of KAR2, CPY, and a-factor are compared in the UCSP-1 transfected and untransfected sec16/ubc6 cells labeled with  $^{35}\text{S}$ -methionine. Proteins are immunoprecipitated with antibodies to KAR2, CPY, and a-factor and separated by immunoelectrophoresis. The accumulation of precursor proteins in UCSP-1 transfected cells is a measure of the UCSP-1 activity in these cells.

### **UCSP-2**

UCSP-2 activity may be measured by degradation of a fusion protein containing ubiquitin conjugated through its C-terminal glycine to UCSP-2. UbCEP fusion proteins are rapidly degraded to free Ub and CEP in incubations containing cell-free rabbit reticulocyte extracts (Monia, et al., supra). This extract contains enzymes required for Ub processing and conjugation of Ub with target proteins. A suitable vector must first be constructed for expression of the Ub-UCSP-2 fusion protein in *E. coli* or *S. cerevisiae*. The purified Ub-UCSP-2 is then incubated in a reaction buffer (50 mM Tris-HCl, pH 7.5, 1 mM dithiothreitol) containing rabbit reticulocyte extract. Reactions are carried out at 37°C for 20 to 40 minutes. and are stopped by heating to 68°C for 5 minutes In the presence of 0.1% SDS. Proteins are separated by polyacrylamide gel electrophoresis. The amount of free UCSP-2 recovered is proportional to the activity of UCSP-2 in the fusion protein.

## **X Production of UCSP Specific Antibodies**

UCSP that is substantially purified using PAGE electrophoresis (Sambrook, supra), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols. The amino acid sequence deduced from SEQ ID NO:2 or SEQ ID NO:4 is  
5 analyzed using DNASTAR software (DNASTAR Inc) to determine regions of high immunogenicity and a corresponding oligopolypeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions, is described by Ausubel et al. (supra), and others.

Typically, the oligopeptides are 15 residues in length, synthesized using an Applied  
10 Biosystems Peptide Synthesizer Model 431A using fmoc-chemistry, and coupled to keyhole limpet hemocyanin (KLH, Sigma, St. Louis, MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS; Ausubel et al., supra). Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity, for example, by binding the peptide to plastic, blocking  
15 with 1% BSA, reacting with rabbit antisera, washing, and reacting with radioiodinated, goat anti-rabbit IgG.

## **XI Purification of Naturally Occurring UCSP Using Specific Antibodies**

Naturally occurring or recombinant UCSP is substantially purified by immunoaffinity chromatography using antibodies specific for UCSP. An immunoaffinity column is constructed  
20 by covalently coupling UCSP antibody to an activated chromatographic resin, such as CnBr-activated Sepharose (Pharmacia & Upjohn). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing UCSP is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of UCSP (e.g., high ionic strength  
25 buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/UCSP binding (eg, a buffer of pH 2-3 or a high concentration of a chaotrope, such as urea or thiocyanate ion), and UCSP is collected.

## **XII Identification of Molecules Which Interact with UCSP**

UCSP or biologically active fragments thereof are labeled with <sup>125</sup>I Bolton-Hunter  
30 reagent (Bolton et al. (1973) Biochem. J. 133:529). Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled UCSP, washed and any wells with labeled UCSP complex are assayed. Data obtained using different concentrations of UCSP are used to calculate values for the number, affinity, and association of UCSP with the candidate

molecules.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit  
5 of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

46  
SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: INCYTE PHARMACEUTICALS, INC.
- (ii) TITLE OF THE INVENTION: UBIQUITIN CONJUGATION PROTEINS
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- (B) STREET: 3174 Porter Drive
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) PCT APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Herewith
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/861,269
- (B) FILING DATE: 21-MAY-1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Billings, Lucy J.
- (B) REGISTRATION NUMBER: 36,749
- (C) REFERENCE/DOCKET NUMBER: PF-0302 PCT
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 650-855-0555
- (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: KERANOT02
- (B) CLONE: 2029018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Ser	Thr	Ser	Ser	Lys	Arg	Ala	Pro	Thr	Thr	Ala	Thr	Gln	Arg
1				5					10					15	
Leu	Lys	Gln	Asp	Tyr	Leu	Arg	Ile	Lys	Lys	Asp	Pro	Val	Pro	Tyr	Ile
			20					25					30		
Cys	Ala	Glu	Pro	Leu	Pro	Ser	Asn	Ile	Leu	Glu	Trp	His	Tyr	Val	Val
			35				40					45			
Arg	Gly	Pro	Glu	Met	Thr	Pro	Tyr	Glu	Gly	Gly	Tyr	Tyr	His	Gly	Lys
	50					55					60				
Leu	Ile	Phe	Pro	Arg	Glu	Phe	Pro	Phe	Lys	Pro	Pro	Ser	Ile	Tyr	Met
65					70				75					80	



## 47

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Ile Thr Pro Asn Gly Arg Phe Lys Cys Asn Thr Arg Leu Cys Leu Ser
      85          90          95
Ile Thr Asp Phe His Pro Asp Thr Trp Asn Pro Ala Trp Ser Val Ser
      100        105        110
Thr Ile Leu Thr Gly Leu Leu Ser Phe Met Val Glu Lys Gly Pro Thr
      115        120        125
Leu Gly Ser Ile Glu Thr Ser Asp Phe Thr Lys Arg Gln Leu Ala Val
      130        135        140
Gln Ser Leu Ala Phe Asn Leu Lys Asp Lys Val Phe Cys Glu Leu Phe
      145        150        155        160
Pro Glu Val Val Glu Ile Lys Gln Lys Gln Lys Ala Gln Asp Glu
      165        170        175
Leu Ser Ser Arg Pro Gln Thr Leu Pro Leu Pro Asp Val Val Pro Asp
      180        185        190
Gly Glu Thr His Leu Val Gln Asn Gly Ile Gln Leu Leu Asn Gly His
      195        200        205
Ala Pro Gly Ala Val Pro Asn Leu Ala Gly Leu Gln Gln Ala Asn Arg
      210        215        220
His His Gly Leu Leu Gly Gly Ala Leu Ala Asn Leu Phe Val Ile Val
      225        230        235        240
Gly Phe Ala Ala Phe Ala Tyr Thr Val Lys Tyr Val Leu Arg Ser Ile
      245        250        255
Ala Gln Glu

```

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KERANOT02
- (B) CLONE: 2029018

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

GATGAGCAGC ACCAGCAGTA AGAGGGCTCC GACCACGGCA ACCCAGAGGC TGAAGCAGGA      60
CTACCTTCGC ATTAAGAAAG ACCCGGTGCC TTACATCTGT GCCGAGCCCC TCCCTTCGAA      120
TATTCTCGAG TGGCACTATG TCGTCCGAGG CCCAGAGATG ACCCCTTATG AAGGTGGCTA      180
TTATCATGGA AAAC TAATTT TTCCCAGAGA ATTTCTTTT AAACCTCCCA GTATCTATAT      240
GATCACTCCC AACGGGAGGT TTAAGTGCAA CACGAGCTG TGTCTTTCTA TCACGGATTT      300
CCACCCGGAC ACGTGAACG CCGCCTGGTC TGTCTCCACC ATCTGACTG GGCTCCTGAG      360
CTTCATGGTG GAGAAGGGCC CCACCCTGGG CAGTATAGAG ACGTCGGACT TCACGAAAAG      420
ACAACTGGCA GTGCAGAGTT TAGCATTTAA TTTGAAAGAT AAAGTCTTTT GTGAATTATT      480
TCCTGAAGTC GTGGAGGAGA TTAAACAAAA ACAGAAAGCA CAAGACGAAC TCAGTAGCAG      540
ACCCAGACT CTCCCCTTGC CAGACGTGGT TCCAGACGGG GAGACGCACC TCGTCCAGAA      600
CGGGATTTCAG CTGCTCAACG GGCATGCGCC GGGGGCCGTC CCAAACCTCG CAGGGCTCCA      660
GCAGGCCAAC CGGCACCACG GACTCCTGGG TGGCGCCCTG GCGAACTTGT TTGTGATAGT      720
TGGGTTTGCA GCCTTTGCTT ACACGGTCAA GTACGTGCTG AGGAGCATCG CGCAGGAGTG      780
AGGCCCAGGC GCCGAGACCC AAGGCGCCAC TGAGGGCACC GCGCACCAGA GCCTGACCTC      840
GGCAGGCTGG ACACACTGCC CAGCACAGGC AGACCCACCA GGCTCCTAGG TTTAGCTTTT      900
AAAAACCTGA AAGGGGAAGC AAAAACCAAA ATGTGTGACT GGGCTTTGGA GGAGACTGGA      960
GCCTCAGCCC TGTCTGGCC ACGGGCCGCT GGGGCTGGTG TGGGTGGGCC TTGTGTGCTG      1020
GATTTGTAGC TTATCTTCCG TGTTGTCTTT GGACCTGTTT TAGTAAACCC GTTTTTTCATT      1080
TT

```

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## 48

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT09  
(B) CLONE: 2151473

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Ala Gln Glu Thr Asn His Ser Gln Val Pro Met Leu Cys Ser Thr
 1           5           10           15
Gly Cys Gly Phe Tyr Gly Asn Pro Arg Thr Asn Gly Met Cys Ser Val
          20           25           30
Cys Tyr Lys Glu His Leu Gln Arg Gln Asn Ser Ser Asn Gly Arg Ile
          35           40           45
Ser Pro Pro Ala Thr Ser Val Ser Ser Leu Ser Glu Ser Leu Pro Val
          50           55           60
Gln Cys Thr Asp Gly Ser Val Pro Glu Ala Gln Ser Ala Leu Asp Ser
65           70           75           80
Thr Ser Ser Ser Met Gln Pro Ser Pro Val Ser Asn Gln Ser Leu Leu
          85           90           95
Ser Glu Ser Val Ala Ser Ser Gln Leu Asp Ser Thr Ser Val Asp Lys
          100          105          110
Ala Val Pro Glu Thr Glu Asp Val Gln Ala Ser Val Ser Asp Thr Ala
          115          120          125
Gln Gln Pro Ser Glu Glu Gln Ser Lys Ser Leu Glu Lys Pro Lys Gln
          130          135          140
Lys Lys Asn Arg Cys Phe Met Cys Arg Lys Lys Val Gly Leu Thr Gly
145          150          155          160
Phe Glu Cys Arg Cys Gly Asn Val Tyr Cys Gly Val His Arg Tyr Ser
          165          170          175
Asp Val His Asn Cys Ser Tyr Asn Tyr Lys Ala Asp Ala Ala Glu Lys
          180          185          190
Ile Arg Lys Glu Asn Pro Val Val Val Gly Glu Lys Ile Gln Lys Ile
          195          200          205

```

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT09  
(B) CLONE: 2151473

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

TCGGCGGCAT TACCTGTACC CATTACCCGG CGGCTACCGG CGGCGGCGCG CAGTGTTTCAG      60
GCGGAGAGAC CCGCCGCCAG GAATTGAATC TGAAGTCTGC TGCAGTAAAA CACAGAAGGC      120
TTTAAAATGT TTTCTTGCAT AAAATTCAAA ACTTTTAAGT AGCTGCTTAT GAGAATAGGG      180
AAGGCAGAAA GCTAATGTCT GTCTCAAGAT ACAGGACAGC TGTTTGCTCA TCAACCTCAA      240
CTGTGTGTGC AACTGAGGAA CATGGCTCAA GAAACTAATC ACAGCCAAGT GCCTATGCTT      300
TGTTCCACTG GCTGTGGATT TTATGGAAAC CCTCGTACAA ATGGCATGTG TTCAGTATGC      360
TATAAAGAAC ATCTTCAAAG ACAGAATAGT AGTAATGGTA GAATAAGCCC ACCTGCAACC      420
TCTGTCTAGT GTCTGTCTGA ATCTTTACCA GTTCAATGCA CAGATGGCAG TGTGCCAGAA      480
GCCCAGTCAG CATTAGACTC TACATCTTCA TCTATGCAGC CCAGCCCTGT ATCAAATCAG      540
TCAC'TTTTAT CAGAATCTGT AGCATCTTCT CAATTGGACA GTACATCTGT GGACAAAGCA      600
GTACCTGAAA CAGAAGATGT GCAGGCTTCA GTATCAGACA CAGCACAGCA GCCATCTGAA      660
GAGCAAAGCA AGTCTCTTGA AAAACCGAAA CAAAAAAGA ATCGCTGTTT CATGTGCAGG      720
AAGAAAGTGG GACTTACTGG GTTTGAATGC CGGTGTGGAA ATGTTTACTG TGGTGTACAC      780
CGTTACTCAG ATGTACACAA TTGCTCTTAC AATTACAAAG CCGATGCTGC TGAGAAAATC      840
AGAAAAGAAA ATCCAGTAGT TGTTGGTGAA AAGATCCAAA AGATTTGAAC TCCTGCTGGA      900
ATACAAAATT CTTGAGCATC TGCAAATAA AAATTGACTT GAGGTTTTTT TTTTCCTAGT      960
CATTGGGAAT GTAGAGCAGT GTATCTTGCA TGTCATCGGA AGAATAGATT TTTGTTTTGG      1020
TTTTGTTTGG AAAATGACTC TGAACATTTA TTTCCATTGC AATTCTCTGT GCTGAGGAGA      1080

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## 49

CTTAAACTTT	ACAAGTATTA	TCCTTTTAAAG	ATCATTTTAA	TTTTAGTTGA	GTGCAGAGGG	1140
CTTTTATAAC	AAACCGTGCA	GAAATTTTGG	AGGGCTGTGA	TTTTTCCAGT	ATTAAAC	1197

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: 397581  
(B) CLONE: GenBank

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met 1	Ala	Thr	Lys	Gln 5	Ala	His	Lys	Arg	Leu 10	Thr	Lys	Glu	Tyr	Lys 15	Leu
Met	Val	Glu	Asn 20	Pro	Pro	Pro	Tyr	Ile 25	Leu	Ala	Arg	Pro	Asn 30	Glu	Asp
Asn	Ile	Leu 35	Glu	Trp	His	Tyr	Ile 40	Ile	Thr	Gly	Pro	Ala 45	Asp	Thr	Pro
Tyr	Lys 50	Gly	Gly	Gln	Tyr	His 55	Gly	Thr	Leu	Thr	Phe 60	Pro	Ser	Asp	Tyr
Pro 65	Tyr	Lys	Pro	Pro	Ala 70	Ile	Arg	Met	Ile	Thr 75	Pro	Asn	Gly	Arg	Phe 80
Lys	Pro	Asn	Thr	Arg 85	Leu	Cys	Leu	Ser	Met 90	Ser	Asp	Tyr	His	Pro	Asp 95
Thr	Trp	Asn 100	Pro	Gly	Trp	Ser	Val	Ser 105	Thr	Ile	Leu	Asn	Gly 110	Leu	Leu
Ser	Phe	Met 115	Thr	Ser	Asp	Glu	Ala 120	Thr	Thr	Gly	Ser	Ile 125	Thr	Thr	Ser
Asp	His 130	Gln	Lys	Lys	Thr	Leu 135	Ala	Arg	Asn	Ser	Ile 140	Ser	Tyr	Asn	Thr
Phe 145	Gln	Asn	Val	Arg	Phe 150	Lys	Leu	Ile	Phe	Pro 155	Glu	Val	Val	Gln	Glu 160
Asn	Val	Glu	Thr	Leu 165	Glu	Lys	Arg	Lys	Leu 170	Asp	Glu	Gly	Asp	Ala	Ala 175
Asn	Thr	Gly	Asp 180	Glu	Thr	Glu	Asp	Pro 185	Phe	Thr	Lys	Ala	Ala 190	Lys	Glu
Lys	Val 195	Ile	Ser	Leu	Glu	Glu	Ile 200	Leu	Asp	Pro	Glu	Asp 205	Arg	Ile	Arg
Ala 210	Glu	Gln	Ala	Leu	Arg	Gln 215	Ser	Glu	Asn	Asn	Ser	Lys	Lys	Asp	Gly
Lys 225	Glu	Pro	Asn	Asp 230	Ser	Ser	Ser	Met	Val	Tyr 235	Ile	Gly	Ile	Ala	Ile 240
Phe	Leu	Phe	Leu	Val 245	Gly	Leu	Phe	Met	Lys 250						

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 1749704

## 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr	Lys	Arg	Leu	Met	Lys	Glu	Tyr	Leu	Ala	Leu	Gln	Lys	Asn	Pro	Phe	1	5	10	15
Glu	Leu	Val	Asp	Ala	Lys	Pro	Ala	Thr	Glu	Asn	Ile	Leu	Glu	Trp	His	20	25	30	
Tyr	Ile	Ile	Thr	Gly	Pro	Pro	Asp	Thr	Pro	Tyr	Glu	Gly	Gln	Tyr		35	40	45	
His	Gly	Thr	Leu	Ile	Phe	Pro	Pro	Asp	Tyr	Pro	Phe	Lys	Pro	Pro	Ala	50	55	60	
Ile	Arg	Met	Ile	Thr	Pro	Ser	Gly	Arg	Phe	Gln	Thr	Asn	Thr	Arg	Leu	65	70	75	80
Cys	Leu	Ser	Phe	Ser	Asp	Phe	His	Pro	Lys	Ser	Trp	Asn	Pro	Ser	Trp	85	90	95	
Met	Val	Ser	Thr	Ile	Leu	Val	Gly	Leu	Val	Ser	Phe	Met	Thr	Ser	Asp	100	105	110	
Glu	Ile	Thr	Thr	Gly	Gly	Ile	Val	Thr	Ser	Glu	Ser	Thr	Arg	Arg	Thr	115	120	125	
Tyr	Ala	Lys	Asp	Thr	Lys	Arg	Phe	Asn	Ile	Met	Asp	Asn	Pro	Lys	Phe	130	135	140	
Leu	Ile	Met	Phe	Pro	Glu	Leu	Ile	Asp	Lys	Asn	Arg	Glu	Asp	Ile	Ala	145	150	155	160
Lys	Ala	Ala	Ala	Glu	Ala	Ala	Leu	Ile	Glu	Pro	Gln	Gln	Ile	His	Ser	165	170	175	
Thr	Pro	Val	Ser	Ser	Asn	Glu	Cys	Lys	Lys	Asn	Glu	Pro	Phe	Asn	Ser	180	185	190	
Lys	Gln	Ser	Trp	Val	Lys	Ser	Arg	Trp	Ser	Ile	Ala	Val	Leu	Val	Phe	195	200	205	
Phe	Ala	Leu	Ala	Leu	Ala	Arg	Phe	Phe	Gly	Ala	Asp	Ser				210	215	220	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1279278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Asn	Glu	Gln	Gln	Gln	Ala	Gln	Thr	Ala	Pro	Ser	Cys	Arg	Ala	1	5	10	15
Gly	Cys	Gly	Phe	Phe	Gly	Ala	Ser	Ala	Thr	Glu	Gly	Tyr	Cys	Ser	Gln	20	25	30	
Cys	Phe	Lys	Asn	Thr	Leu	Lys	Arg	Gln	Gln	Asp	Thr	Val	Arg	Leu	Thr	35	40	45	
Ser	Pro	Val	Val	Ser	Pro	Ser	Ser	Met	Ala	Ala	Thr	Ser	Ser	Ala	Leu	50	55	60	
Lys	Ser	Glu	Pro	Ser	Ser	Val	Asp	Met	Cys	Met	Lys	Ala	Ala	Val	Ser	65	70	75	80
Val	Ser	Asp	Glu	Thr	Ala	Lys	Met	Asp	Cys	Glu	Asp	Ile	Ile	Asn	Val	85	90	95	
Cys	Asp	Gln	Ile	Asn	Asp	Asp	Ser	Val	Thr	Val	Ala	Glu	Ser	Thr	Ala	100	105	110	
Pro	Thr	Thr	Ile	Thr	Val	Asp	Val	Pro	Val	Pro	Val	Lys	Lys	Ala	Asn	115	120	125	
Arg	Cys	His	Met	Cys	Lys	Lys	Arg	Val	Gly	Leu	Thr	Gly	Phe	Ser	Cys	130	135	140	
Arg	Cys	Gly	Gly	Leu	Tyr	Cys	Gly	Asp	His	Arg	Tyr	Asp	Gln	Ala	His	145	150	155	160
Asn	Cys	Gln	Phe	Asp	Tyr	Lys	Thr	Met	Glu	Arg	Glu	Thr	Ile	Arg	Lys	165	170	175	

51

Asn Asn Pro Val Val Val Ser Asp Lys Val Gln Arg Ile  
 180 185

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 998680

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys	Arg	Cys	Gly	Asn	Leu	Phe	Cys	Gly	Leu	His	Arg	Tyr	Ser	Asp	Lys
1				5					10					15	
His	Asn	Cys	Pro	Tyr	Asp	Tyr	Lys	Ala	Glu	Ala	Ala	Ala	Lys	Ile	Arg
			20					25					30		
Lys	Glu	Asn	Pro	Val	Val	Val	Ala	Glu	Lys	Ile	Gln	Arg	Ile		
		35					40					45			

What is claimed is:

1. A substantially purified ubiquitin conjugation system protein comprising the amino acid sequence of SEQ ID NO:1 or fragments thereof.
2. An isolated and purified polynucleotide sequence encoding the ubiquitin  
5 conjugation system protein of claim 1.
3. A polynucleotide sequence which hybridizes under stringent conditions to the polynucleotide sequence of claim 2.
4. A hybridization probe comprising the polynucleotide sequence of claim 2.
5. An isolated and purified polynucleotide sequence comprising SEQ ID NO:2 or  
10 variants thereof.
6. A polynucleotide sequence which is complementary to the polynucleotide sequence of claim 2 or variants thereof.
7. A hybridization probe comprising the polynucleotide sequence of claim 6.
8. An expression vector containing the polynucleotide sequence of claim 2.
- 15 9. A host cell containing the vector of claim 8.
10. A method for producing a polypeptide comprising the amino acid sequence of SEQ ID NO:1 the method comprising the steps of:
  - a) culturing the host cell of claim 9 under conditions suitable for the expression of the polypeptide; and
  - 20 b) recovering the polypeptide from the host cell culture.
11. A pharmaceutical composition comprising a substantially purified ubiquitin conjugation system protein having an amino acid sequence of claim 1 in conjunction with a suitable pharmaceutical carrier.
12. A purified antibody which binds specifically to the polypeptide of claim 1.
- 25 13. A purified agonist which modulates the activity of the polypeptide of claim 1.
14. A purified antagonist which decreases the activity of the polypeptide of claim 1.
15. A method for treating cancer comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 11.
16. A method for treating a smooth muscle disorder comprising administering to a  
30 subject in need of such treatment an effective amount of the purified antagonist of claim 14.
17. A method for treating a viral disease comprising administering to a subject in need of such treatment an effective amount of the purified antagonist of claim 14.

18. A method for detection of a polynucleotide encoding a ubiquitin conjugation system protein in a biological sample comprising the steps of:

a) hybridizing the polynucleotide of claim 6 to nucleic acid material of a biological sample, thereby forming a hybridization complex; and

5 b) detecting said hybridization complex, wherein the presence of said complex correlates with the presence of a polynucleotide encoding a ubiquitin conjugation system protein in said biological sample.

19. A substantially purified ubiquitin conjugation system protein comprising the amino acid sequence of SEQ ID NO:3 or fragments thereof.

10 20. An isolated and purified polynucleotide sequence encoding the ubiquitin conjugation system protein of claim 19.

21. A polynucleotide sequence which hybridizes under stringent conditions to the polynucleotide sequence of claim 20.

22. A hybridization probe comprising the polynucleotide sequence of claim 20.

15 23. An isolated and purified polynucleotide sequence comprising SEQ ID NO:4 or variants thereof.

24. A polynucleotide sequence which is complementary to the polynucleotide sequence of claim 20 or variants thereof.

25. A hybridization probe comprising the polynucleotide sequence of claim 24.

20 26. An expression vector containing the polynucleotide sequence of claim 20.

27. A host cell containing the vector of claim 26.

28. A method for producing a polypeptide comprising the amino acid sequence of SEQ ID NO:3 the method comprising the steps of:

a) culturing the host cell of claim 27 under conditions suitable for the  
25 expression of the polypeptide; and

b) recovering the polypeptide from the host cell culture.

29. A pharmaceutical composition comprising a substantially purified ubiquitin conjugation system protein having an amino acid sequence of claim 19 in conjunction with a suitable pharmaceutical carrier.

30 30. A purified antibody which binds specifically to the polypeptide of claim 19.

31. A purified agonist which modulates the activity of the polypeptide of claim 19.

32. A purified antagonist which decreases the activity of the polypeptide of claim 19.

33. A method for treating cancer comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 29.

34. A method for treating an immune disorder comprising administering to a subject in need of such treatment an effective amount of the purified antagonist of claim 32.

5 35. A method for detection of a polynucleotide encoding a ubiquitin conjugation system protein in a biological sample comprising the steps of:

a) hybridizing the polynucleotide of claim 24 to nucleic acid material of a biological sample, thereby forming a hybridization complex; and

b) detecting said hybridization complex, wherein the presence of said  
10 complex correlates with the presence of a polynucleotide encoding a ubiquitin conjugation system protein in said biological sample.



9	18	27	36	45	54
NNG ATG AGC AGC ACC AGC AGT AAG AGG GCT CCG ACC ACC GCA ACC CAG AGG CTG					
M S S T S S K R A P T T A T Q R L					
63	72	81	90	99	108
AAG CAG GAC TAC CTT CGC ATT AAG AAA GAC CCG GTG CCT TAC ATC TGT GCC GAG					
K Q D Y L R I K K D P V P Y I C A E					
117	126	135	144	153	162
CCC CTC CCT TCG AAT ATT CTC GAG TGG CAC TAT GTC GTC CGA GGC CCA GAG ATG					
P L P S N I L E W H Y V V R G P E M					
171	180	189	198	207	216
ACC CCT TAT GAA GGT GGC TAT TAT CAT GGA AAA CTA ATT TTT CCC AGA GAA TTT					
T P Y E G G Y Y H G K L I F P R E F					
225	234	243	252	261	270
CCT TTC AAA CCT CCC AGT ATC TAT ATG ATC ACT CCC AAC GGG AGG TTT AAG TGC					
P F K P P S I I Y M I T P N G R F K C					
279	288	297	306	315	324
AAC ACC AGG CTG TGT CTT TCT ATC ACG GAT TTC CAC CCG GAC ACG TGG AAC CCG					
N T R L C L S I T D F H P D T W N P					
333	342	351	360	369	378
GCC TGG TCT GTC TCC ACC ATC CTG ACT GGG CTC CTG AGC TTC ATG GTG GAG AAG					
A W S V S T I L T G L L S F M V E K					

FIGURE 1A

387	405	414	423	432
GGC CCC ACC CTG GGC AGT ATA GAG ACG TCG GAC TTC	ACG TCG GAC TTC	ACG AAA AGA CAA CTG GCA		
G P T L G S I E T S D F F T K R Q L A				
441	450	468	477	486
GTG CAG AGT TTA GCA TTT AAT TTG AAA GAT AAA GTC TTT TGT GAA TTA TTT CCT				
V Q S L A F N L K D K V F C E L F P				
495	504	513	522	531
GAA GTC GTG GAG GAG ATT AAA CAA AAA CAG AAA GCA CAA GAC GAA CTC AGT AGC				
E V V E E I K Q K Q K A Q D E L S S				
549	558	567	576	585
AGA CCC CAG ACT CTC CCC TTG CCA GAC GTG GTT CCA GAC GAC GGG GAG ACG CAC CTC				
R P Q T L P L P D V V P P D G E T H L				
603	612	621	630	639
GTC CAG AAC GGG ATT CAG CTG CTC AAC GGG CAT GCG CCG GGG GCG GTC CCA AAC				
V Q N G I Q L L L N G H A P G A V P N				
657	666	675	684	693
CTC GCA GGG CTC CAG CAG GCC AAC CCG CAC CAC GGA CTC CTG GGT GGC GCC CTG				
L A G L Q Q A N R H H G L L G G A L				
711	720	729	738	747
GCG AAC TTG TTT GTG ATA GTT GGG TTT GCA GCC TTT GCT TAC ACG GTC AAG TAC				
A N L F V I V G G F A A A F A Y T V K Y				

FIGURE 1B

765 774 783 792 801 810  
 GTG CTG AGG AGC ATC GCG CAG GAG TGA GGC CCA GGC GCC GAG ACC CAA GGC GCC  
 V L R S I A Q E  
 819 828 837 846 855 864  
 ACT GAG GGC ACC GCG CAC CAG AGC GTG ACC TCG GCA GGC TGG ACA CAC TGC CCA  
 873 882 891 900 909 918  
 GCA CAG GCA GAC CCA CCA GGC TCC TAG GTT TAG CTT TTA AAA ACC TGA AAG GGG  
 927 936 945 954 963 972  
 AAG CAA AAA CCA AAA TGT GTG ACT GGG CTT TGG AGG AGA CTG GAG CCT CAG CCC  
 981 990 999 1008 1017 1026  
 TGT CCT GGC CAC GGC CCG CTG GGC CTG GTG TGG GTG GGC CTT GTG TGC TGG ATT  
 1035 1044 1053 1062 1071 1080  
 TGT AGC TTA TCT TCC GTG TTG TCT TTG GAC CTG TTT TAG TAA ACC CGT TTT TCA  
 TTT T

FIGURE 1C

9	18	27	36	45	54
NNN TCG GCG GCA TTA CCT GTA CCC ATT CAC CGG CGG CTA CCG GCG GCG GCG CGC					
63	72	81	90	99	108
AGT GTT CAG GCG GAG AGA CCC GCC GCC AGG AAT TGA ATC TGA AGT CTG CTG CAG					
117	126	135	144	153	162
TAA AAC ACA GAA GGC TTT AAA ATG TTT TCT TGC ATA AAA TTC AAA ACT TTT AAG					
171	180	189	198	207	216
TAG CTG CTT ATG AGA ATA GGG AAG GCA GAA AGC TAA TGT CTG TCT CAA GAT ACA					
225	234	243	252	261	270
GGA CAG CTG TTT GCT CAT CAA CCT CAA CTG TGT GTG CAA CTG AGG AAC ATG GCT					
					M A
279	288	297	306	315	324
CAA GAA ACT AAT CAC AGC CAA GTG CCT ATG CTT TGT TCC ACT GGC TGT GGA TTT					
Q E T N H S Q V P M L C S T G C G F					
333	342	351	360	369	378
TAT GGA AAC CCT CGT ACA AAT GGC ATG TGT TCA GTA TGC TAT AAA GAA CAT CTT					
Y G N P R T N G M C S V C Y K E H L					

FIGURE 2A

387	396	405	414	423	432
CAA AGA CAG AAT AGT AGT AAT GGT AGA ATA AGC CCA CCT GCA ACC TCT GTC AGT					
Q R Q N S S N G R I S P P A T S V S					
441	450	459	468	477	486
AGT CTG TCT GAA TCT TTA CCA GTT CAA TGC ACA GAT GGC AGT GTG CCA GAA GCC					
S L S E S L P V Q C T D G S V P E A					
495	504	513	522	531	540
CAG TCA GCA TTA GAC TCT ACA TCT TCA TCT ATG CAG CCC AGC CCT GTA TCA AAT					
Q S A L D S T S S S M Q P S V S N					
549	558	567	576	585	594
CAG TCA CTT TTA TCA GAA TCT GTA GCA TCT TCT CAA TTG GAC AGT ACA TCT GTG					
Q S L L S E S V A S S Q L D S T S V					
603	612	621	630	639	648
GAC AAA GCA GTA CCT GAA ACA GAA GAT GTG CAG GCT TCA GTA TCA GAC ACA GCA					
D K A V P E T E D V Q A S V S D T A					
657	666	675	684	693	702
CAG CAG CCA TCT GAA GAG CAA AGC AAG TCT CTT GAA AAA CCG AAA CAA AAA AAG					
Q Q P S E E Q S K S L E K P K Q K K					
711	720	729	738	747	756
AAT CGC TGT TTC ATG TGC AGG AAG AAA GTG GGA CTT ACT GGG TTT GAA TGC CGG					
N R C F M C R K K V G G L T G F E C R					

FIGURE 2B

765	774	783	792	801	810
TGT GGA AAT GTT TAC TGT GGT GTA CAC CGT TAC TCA GAT GTA CAC AAT TGC TCT					
C G N V Y C G V H R Y S D V H N C S					
819	828	837	846	855	864
TAC AAT TAC AAA GCC GAT GCT GCT GAG AAA ATC AGA AAA GAA AAT CCA GTA GTT					
Y N Y K A D A A E K I R K E N P V					
873	882	891	900	909	918
GTT GGT GAA AAG ATC CAA AAG ATT TGA ACT CCT GCT GGA ATA CAA AAT TCT TGA					
V G E K I Q K I					
927	936	945	954	963	972
GCA TCT GCA AAC TAA AAA TTG ACT TGA GGT TTT TTT CCT AGT CAT TGG GAA					
981	990	999	1008	1017	1026
TGT AGA GCA GTG TAT CTT GCA TGT CAT CGG AAG AAT AGA TTT TTG TTT TGG TTT					
1035	1044	1053	1062	1071	1080
TGT TTT GAA AAT GAC TCT TCT GAA CAT TTA TTT CCA TTG CAA TTT CTG TGG CTG AGG					
1089	1098	1107	1116	1125	1134
AGA CTT AAA CTT TAC AAG TAT TAT CCT TTT AAG ATC ATT TTA ATT TTA GTT GAG					

FIGURE 2C

1143 1152 1161 1170 1179 1188  
TGC AGA GGG CTT TTA TAA CAA ACC GTG CAG AAA TTT TGG AGG GCT GTG ATT TTT

1197  
CCA GTA TTA AAC

FIGURE 2D

1	M	S	S	T	S	S	K	R	A	P	T	T	A	T	Q	R	L	K	Q	D	Y	L	R	I	K	K	D	P	V	P	UCSP-1
1	M	A	T	K	Q	A	H	K	-	-	-	-	-	-	-	R	L	T	K	E	Y	K	L	M	V	E	N	P	P	P	g397581
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	L	M	K	E	Y	L	A	L	Q	K	N	P	F	F	g1749704
31	Y	I	C	A	E	P	L	P	S	N	I	L	E	W	H	Y	V	V	R	G	P	E	M	T	P	Y	E	G	G	Y	UCSP-1
24	Y	I	L	A	R	P	N	E	D	N	I	L	E	W	H	Y	I	I	T	G	P	A	D	T	P	Y	K	G	G	Q	g397581
18	L	V	D	A	K	P	A	T	E	N	I	L	E	W	H	Y	I	I	T	G	P	P	D	T	P	Y	E	G	G	Q	g1749704
61	Y	H	G	K	L	I	F	P	R	E	F	P	F	K	P	P	S	I	Y	M	I	T	P	N	G	R	F	K	C	N	UCSP-1
54	Y	H	G	T	L	T	F	P	S	D	Y	P	Y	K	P	P	A	I	R	M	I	T	P	N	G	R	F	K	P	N	g397581
48	Y	H	G	T	L	I	F	P	P	D	Y	P	F	K	P	P	A	I	R	M	I	T	P	S	G	R	F	Q	T	N	g1749704
91	T	R	L	C	L	S	I	T	D	F	H	P	D	T	W	N	P	A	W	S	V	S	T	I	L	T	G	L	L	S	UCSP-1
84	T	R	L	C	L	S	M	S	D	Y	H	P	D	T	W	N	P	G	W	S	V	S	T	I	L	N	G	L	L	S	g397581
78	T	R	L	C	L	S	F	S	D	F	H	P	K	S	W	N	P	S	W	M	V	S	T	I	L	V	G	L	V	S	g1749704
121	F	M	V	E	K	G	P	T	L	G	S	I	E	T	S	D	F	T	K	R	Q	L	A	V	Q	S	L	A	F	N	UCSP-1
114	F	M	T	S	D	E	A	T	T	G	S	I	T	S	D	H	Q	K	K	T	L	A	R	N	S	I	S	Y	N	g397581	
108	F	M	T	S	D	E	I	T	T	G	G	I	V	T	S	E	S	T	R	R	T	Y	A	K	D	T	K	R	F	N	g1749704

FIGURE 3A



151	L	K	D	K	V	-	F	C	E	L	F	P	E	V	V	E	E	I	K	Q	-	-	-	K	Q	K	A	Q	D	E	UCSP-1
144	T	F	Q	N	V	R	F	K	L	I	F	P	E	V	V	Q	E	N	V	E	T	L	E	K	R	K	L	D	E	G	g397581
138	I	M	D	N	P	K	F	L	I	M	F	P	E	L	I	D	K	N	R	E	D	I	A	K	-	-	-	-	-	-	g1749704
177	L	S	S	R	P	Q	T	L	P	L	P	D	V	V	P	D	G	E	T	H	L	V	Q	N	G	I	Q	L	L	N	UCSP-1
174	D	A	A	N	T	G	D	E	T	E	D	P	F	T	K	A	A	K	E	K	V	I	S	L	E	-	E	I	L	D	g397581
162	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	A	A	E	A	A	L	I	E	P	Q	-	Q	I	-	g1749704
207	G	H	A	P	G	A	V	P	N	L	A	G	L	Q	Q	A	N	R	H	H	G	L	L	G	G	A	L	A	-	N	UCSP-1
203	P	E	D	R	I	R	A	E	Q	A	L	R	Q	S	E	N	N	S	K	K	D	-	G	K	E	P	N	D	S	S	g397581
175	H	S	T	P	V	S	S	N	E	C	K	K	N	E	P	F	N	S	K	Q	S	W	V	K	S	R	W	S	I	A	g1749704
236	L	F	V	I	V	G	F	A	A	F	A	Y	T	V	K	Y	V	L	R	S	I	A	Q	E	-	-	-	-	-	-	UCSP-1
232	S	M	V	Y	I	G	I	A	I	F	A	I	F	L	F	-	-	-	-	L	V	G	L	F	M	K	-	-	-	-	g397581
205	V	L	V	F	F	A	L	A	L	A	R	F	-	-	-	-	-	-	F	G	A	-	-	D	S	-	-	-	-	-	g1749704

FIGURE 3B

1	M	A	Q	E	T	N	H	S	Q	V	P	M	L	C	S	T	G	C	G	F	Y	G	N	P	R	T	N	G	M	C	UCSP-2
1	M	E	N	E	Q	Q	Q	A	Q	T	A	P	S	C	R	A	G	C	G	F	F	G	A	S	A	T	E	G	Y	C	g1279278
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g998680
31	S	V	C	Y	K	E	H	L	Q	R	Q	N	S	S	N	G	R	I	S	P	P	A	T	S	V	S	S	L	S	E	UCSP-2
31	S	Q	C	F	K	N	T	L	K	R	Q	Q	D	T	-	V	R	L	T	S	P	V	S	P	S	S	M	A	A	g1279278	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g998680
61	S	L	P	V	Q	C	T	D	G	S	V	P	E	A	Q	S	A	L	D	S	T	S	S	S	M	Q	P	S	P	V	UCSP-2
60	T	-	-	-	-	-	-	-	-	-	-	-	-	S	S	A	L	K	S	E	P	S	S	V	D	-	-	-	M	g1279278	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g998680
91	S	N	Q	S	L	L	S	E	S	V	A	S	S	Q	L	D	S	T	S	V	D	K	A	V	P	E	T	E	D	V	UCSP-2
74	C	M	K	A	A	V	S	V	S	D	E	T	A	K	M	D	C	E	D	I	I	N	V	C	D	Q	I	N	D	D	g1279278
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g998680
121	Q	A	S	V	S	D	T	A	Q	Q	P	S	E	E	Q	S	K	S	L	E	K	P	K	Q	K	K	N	R	C	F	UCSP-2
104	S	V	T	V	A	E	S	T	-	-	A	P	T	T	I	T	V	D	V	P	V	P	V	K	K	A	N	R	C	H	g1279278
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g998680

FIGURE 4A

151	M	C	R	K	K	V	G	L	T	G	F	E	C	R	C	G	N	V	Y	C	G	V	H	R	Y	S	D	V	H	N	UCSP-2
132	M	C	K	K	R	V	G	L	T	G	F	S	C	R	C	G	G	L	Y	C	G	D	H	R	Y	D	Q	A	H	N	g1279278
1	-	-	-	-	-	-	-	-	-	-	-	-	C	R	C	G	N	L	F	C	G	L	H	R	Y	S	D	K	H	N	g998680
181	C	S	Y	N	Y	K	A	D	A	A	E	K	I	R	K	E	N	P	V	V	V	G	E	K	I	Q	K	I	UCSP-2		
162	C	Q	F	D	Y	K	T	M	E	R	E	T	I	R	K	N	N	P	V	V	V	S	D	K	V	Q	R	I	g1279278		
19	C	P	Y	D	Y	K	A	E	A	A	A	K	I	R	K	E	N	P	V	V	V	A	E	K	I	Q	R	I	g998680		

FIGURE 4B

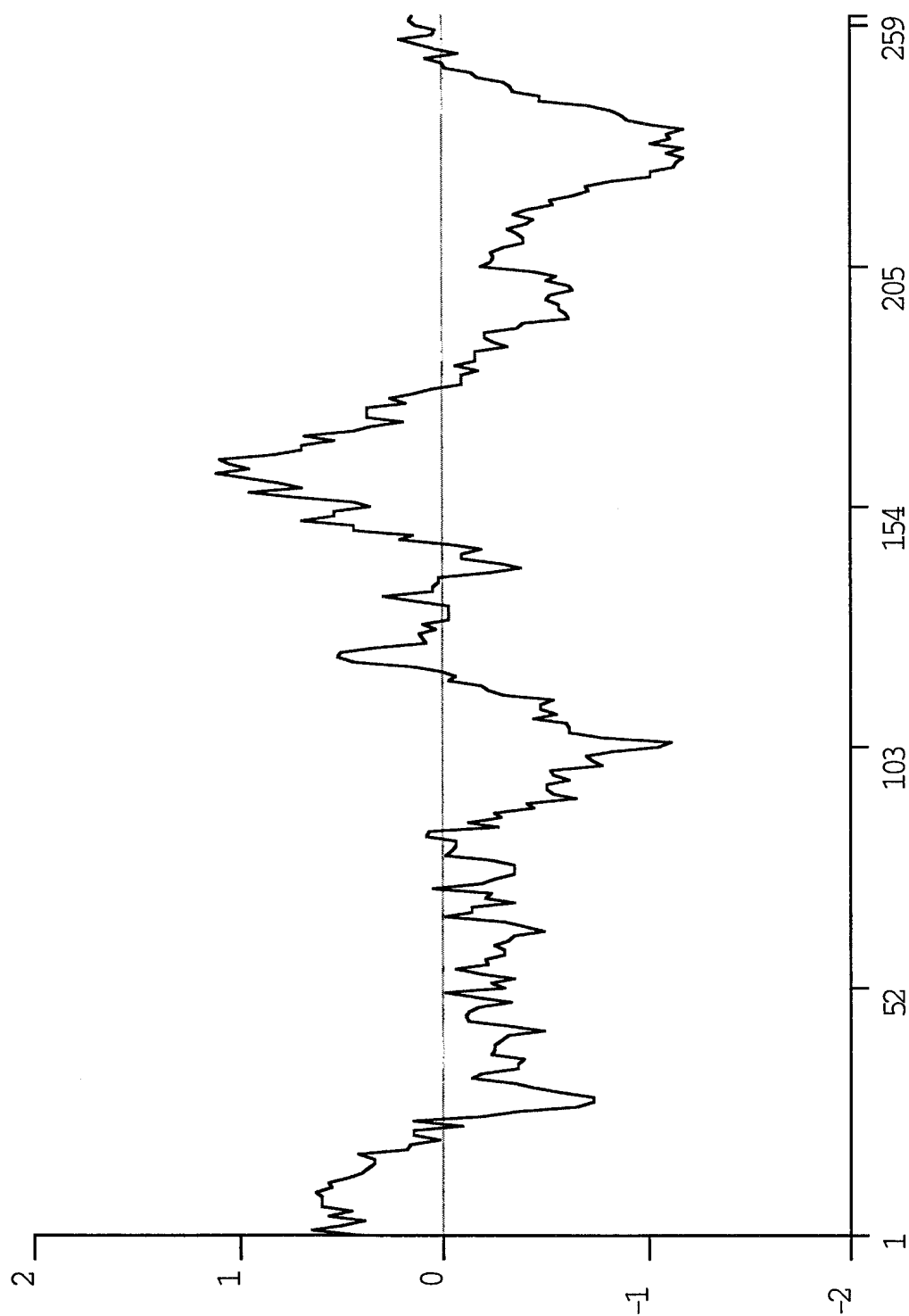


FIGURE 5A

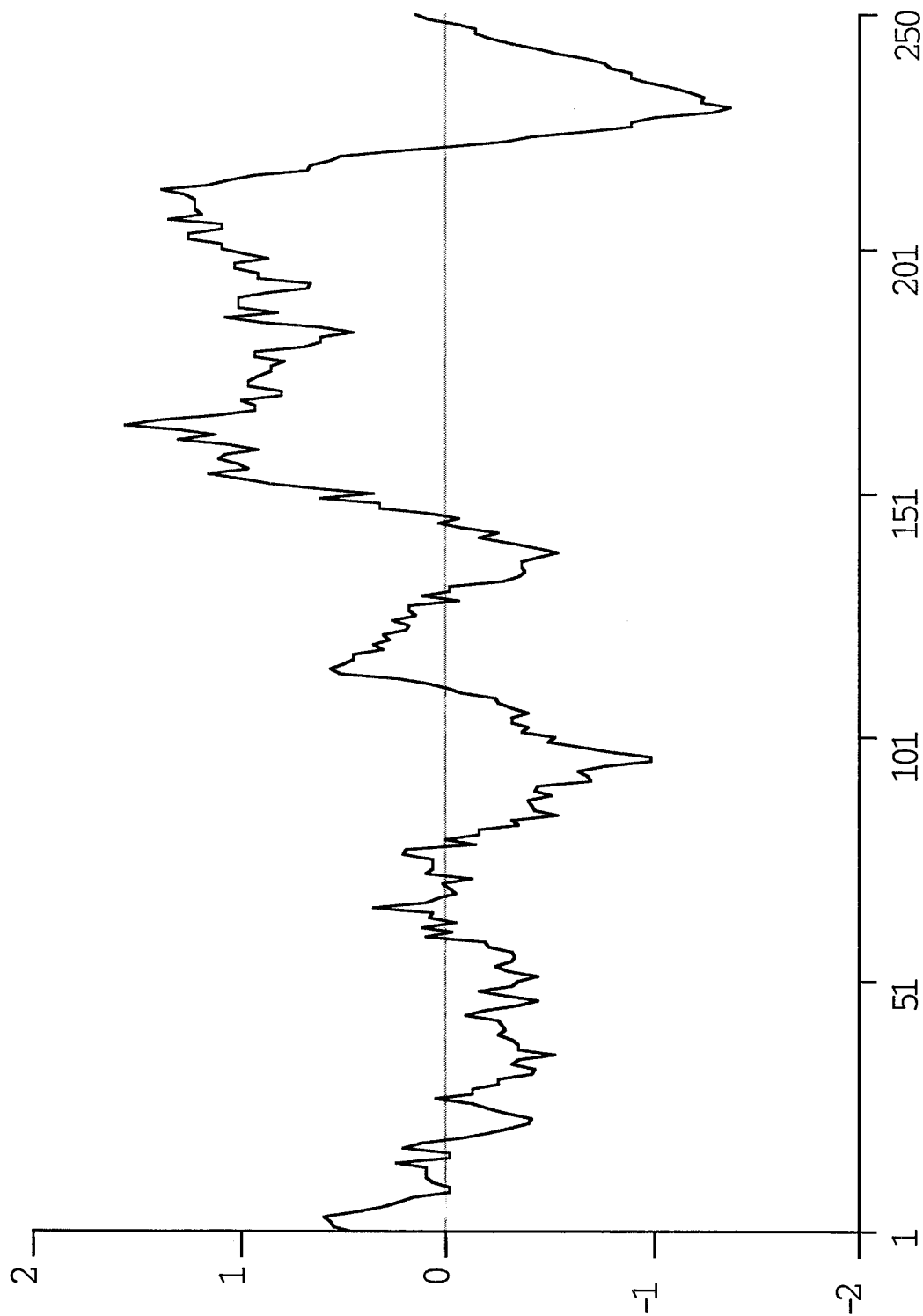


FIGURE 5B

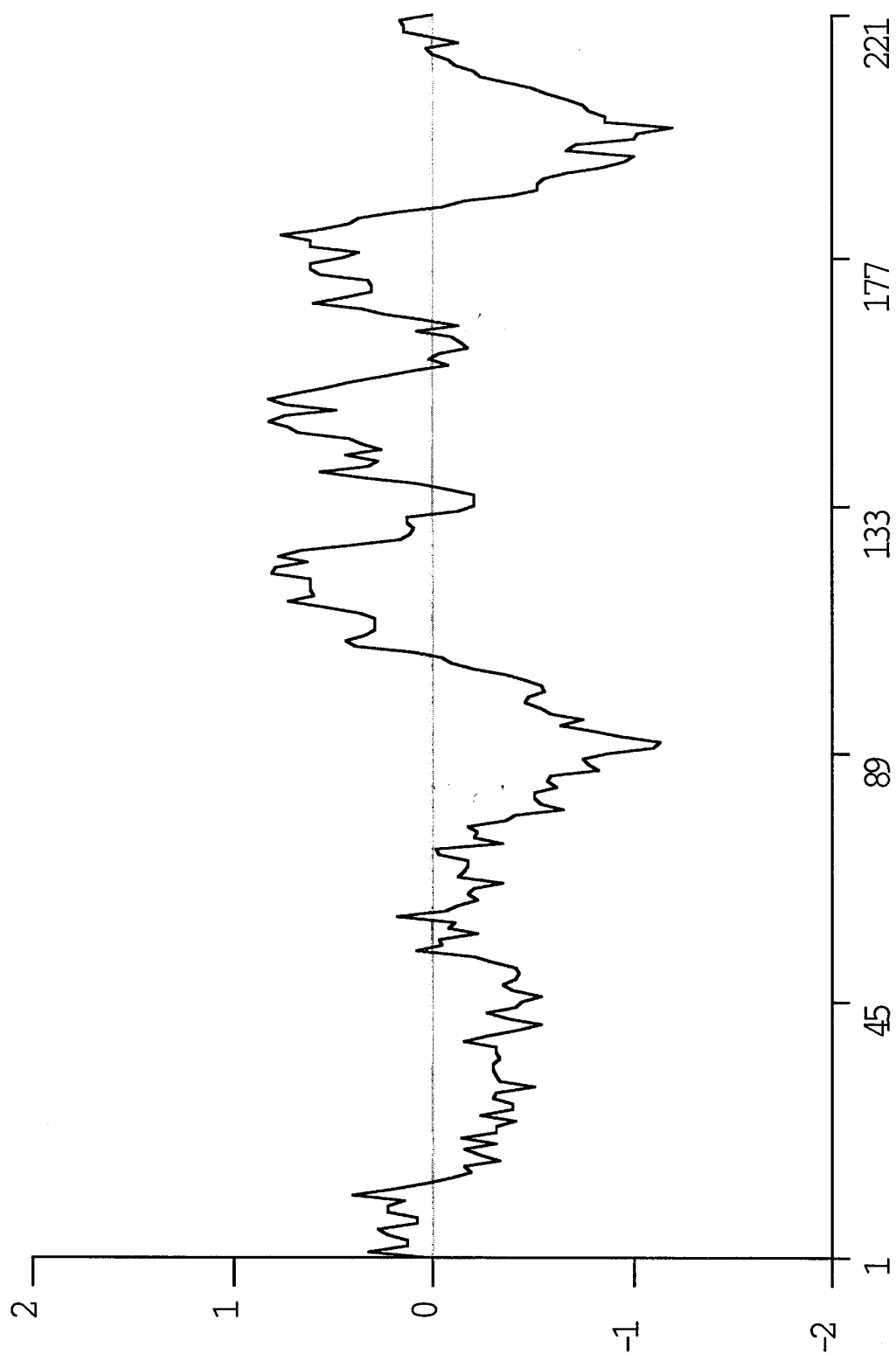


FIGURE 5C

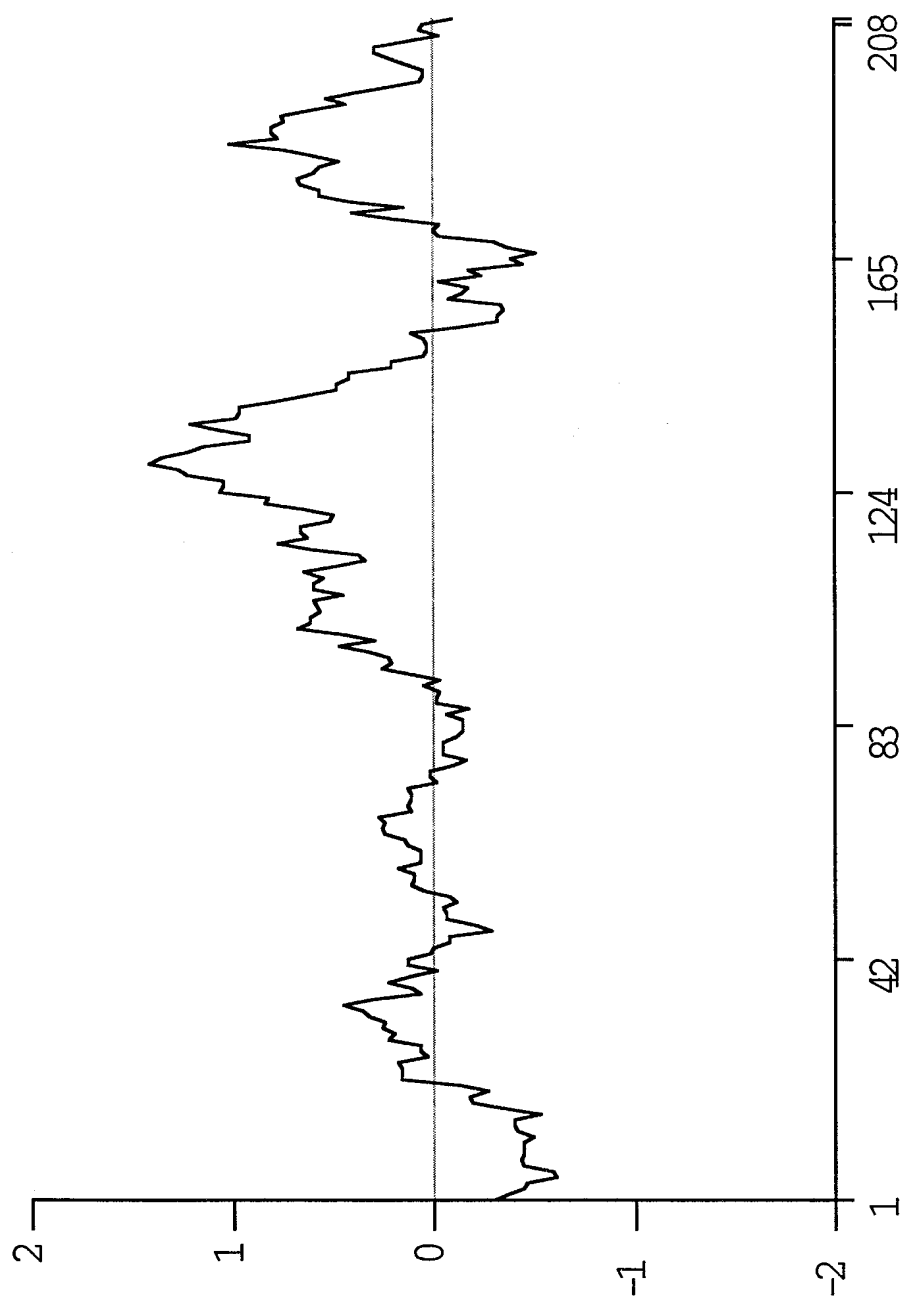


FIGURE 6A

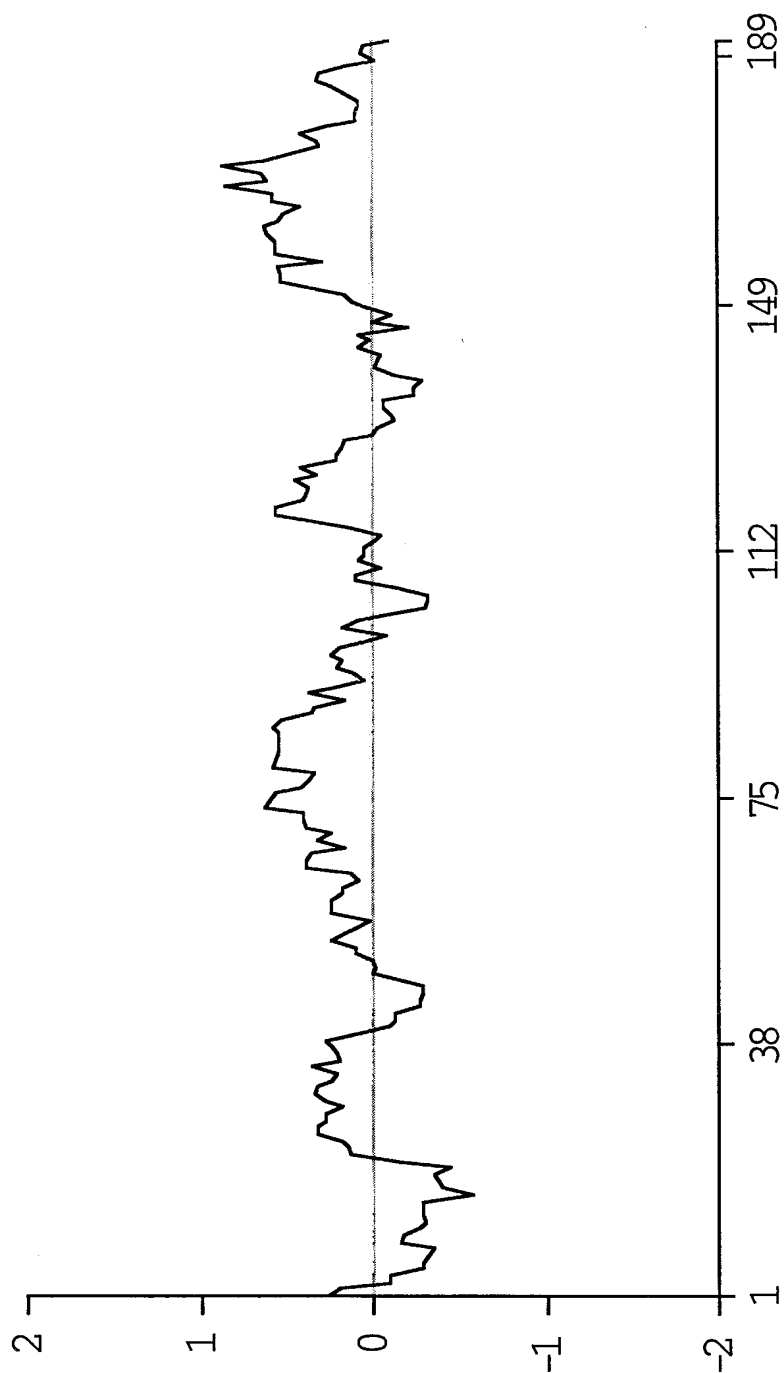


FIGURE 6B



# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10638

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/52 C12N9/00 C12Q1/68 C12N15/11 A61K38/53  
C07K16/40

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12Q A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SOMMER T ET AL: "A protein translocation defect linked to ubiquitin conjugation at the endoplasmic reticulum" NATURE, vol. 365, September 1993, pages 176-179, XP002078649 LONDON GB see figures 1,2	1,2,5-9, 12
X	HILLIER L ET AL: "Homo sapiens cDNA clone 754549 5' similar to SW:UBC6_YEAST P33296 UBIQUITIN-CONJUGATION ENZYME E2-28.4 KD" EMBL Database entry HS1206407 Accession number AA411279; 04 May 1997 XP002078650	3,4
Y	see sequence	1,2,5-9, 12



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

25 September 1998

Date of mailing of the international search report

12/10/1998

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## INTERNATIONAL SEARCH REPORT

Internal Application No

PCT/US 98/10638

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HILLIER L ET AL: "Homo sapiens cDNA clone 417998 5' similar to SW:UBC6_YEAST P33296 UBIQUITIN-CONJUGATION ENZYME E2-28.4 KD" EMBEST Database entry HSW6471 Accession number W90647; 09 JUL 1996 XP002078651	3,4
Y	see sequence	1,2,5-9, 12
X	ADAMS MD ET AL: "Homo sapiens cDNA 5' similar to ubiquitin-conjugating enzyme" EMBEST Database entry HSZZ59197 Accession number AA354073; 18 APR 1997 XP002078652	3,4
Y	see sequence	1,2,5-9, 12
X	HILLIER L ET AL: "Homo sapiens cDNA clone 728300" EMBEST Database entry HS1222367 Accession number AA393664; 19 May 1997 XP002078653	3,4
Y	see sequence	1,2,5-9, 12
X	HILLIER L ET AL: "Homo sapiens cDNA clone 417998" EMBEST Database entry HSW6221 Accession number W90622; 9 Jul 1996 XP002078654	6,7
Y	WILSON R ET AL: "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans" NATURE, vol. 368, 1994, pages 32-38, XP002050139 LONDON GB see the whole document	19,20, 23,26-28
Y	& WILSON R ET AL: "Caenorhabditis elegans" SPTREMBL Database entry Q19723 Accession number Q19723; 01 Nov 1996 see sequence	19,20, 23,26-28
Y	& WILSON R ET AL: "Caenorhabditis elegans" EMINV Database entry Cef22d6 Accession number Z71262; 19 Apr 1996 see sequence	19,20, 23,26-28
X	HILLIER L ET AL: "Homo sapiens cDNA clone 380898" EMBEST Database entry HSA56157 Accession number AA056157; 19 Sep 1996 XP002078655	21,22
Y	see sequence	19,20, 23,26-28

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10638

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HILLIER L ET AL: "Homo sapiens cDNA clone 666240" EMEST Database entry HS1151759 Accession number AA233629; 6 Mar 1997 XP002078656	21,22
Y	see sequence	19,20, 23,26-28
X	----- HILLIER L ET AL: "Homo sapiens cDNA clone 321730 5' similar to PIR:JN0673 ubiquitin-like fusion protein Anla-African clawed frog" EMEST Database entry HS046352 Accession number W33045, 16 May 1996 XP002078657	21,22
Y	see sequence -----	19,20, 23,26-28

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/10638

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 15-17, 33, 34 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 13, 14, 31, 32  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
Said claims relate to agonists and antagonists without giving a further characterization of the claimed matter. In consequence, the scope of said claims is ambiguous and, moreover, their subject-matter is vague and not sufficiently disclosed.
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☒ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-18

Subject-matter relating to SEQ ID NOs 1 and 2, said SEQ Ids referring to an ubiquitin conjugation system UCSP-1 having similarity to UBC6 from *S. cerevisiae*

2. Claims: 19-35

Subject-matter relating to SEQ ID NOs 3 and 4, said SEQ Ids referring to an ubiquitin conjugation system UCSP-2 having similarity to *C. elegans* CEPs